

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 15:03:35 ; Search time 43 Seconds
(without alignments)
1458.915 Million cell updates/sec

Title: US-10-614-076-98

Perfect score: 3406

Sequence: 1 MNPNNRSEHDTIKVTPNSEL.....SFVSNKIVDKIEFIPVQL 652

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|----------|--------------------|
| 1 | 3406 | 100.0 | 652 | 2 I39811 | parasporal crystal |
| 2 | 3212 | 94.3 | 659 | 2 I02228 | parasporal crystal |
| 3 | 2341.5 | 68.7 | 652 | 2 A27233 | parasporal crystal |
| 4 | 2152 | 63.2 | 649 | 1 JH0261 | parasporal crystal |
| 5 | 1127.5 | 33.1 | 1157 | 1 S49247 | parasporal crystal |
| 6 | 1124.5 | 33.0 | 719 | 2 I40590 | parasporal crystal |
| 7 | 1119 | 32.9 | 1138 | 2 A48944 | parasporal crystal |
| 8 | 1100.5 | 32.3 | 719 | 2 I39815 | parasporal crystal |
| 9 | 1091.5 | 32.0 | 719 | 2 I39814 | parasporal crystal |
| 10 | 1091.5 | 32.0 | 719 | 2 S25383 | parasporal crystal |
| 11 | 1072.5 | 31.5 | 1228 | 2 S00873 | parasporal crystal |
| 12 | 1060 | 31.1 | 1160 | 2 I40589 | parasporal crystal |
| 13 | 963.5 | 28.3 | 1154 | 2 S39536 | parasporal crystal |
| 14 | 934.5 | 27.4 | 655 | 2 JC7140 | parasporal crystal |
| 15 | 926.5 | 27.2 | 1189 | 2 S00944 | parasporal crystal |
| 16 | 907.5 | 26.6 | 823 | 2 S04181 | parasporal crystal |
| 17 | 906.5 | 26.6 | 1155 | 2 S02134 | parasporal crystal |
| 18 | 900.5 | 26.4 | 1155 | 2 A26513 | parasporal crystal |
| 19 | 899.5 | 26.4 | 1155 | 2 JD0002 | parasporal crystal |
| 20 | 899.5 | 26.4 | 1156 | 2 A24125 | parasporal crystal |
| 21 | 898.5 | 26.4 | 1174 | 2 A42459 | parasporal crystal |
| 22 | 895.5 | 26.3 | 1155 | 2 I39838 | parasporal crystal |
| 23 | 888 | 26.1 | 1181 | 2 A41052 | parasporal crystal |
| 24 | 886.5 | 26.0 | 1176 | 2 A48970 | parasporal crystal |
| 25 | 876 | 25.7 | 1176 | 2 JT0241 | parasporal crystal |
| 26 | 874 | 25.7 | 934 | 2 A22798 | parasporal crystal |
| 27 | 870 | 25.5 | 1176 | 2 JC2219 | parasporal crystal |
| 28 | 869.5 | 25.5 | 1171 | 2 I40572 | parasporal crystal |
| 29 | 869.5 | 25.5 | 1171 | 2 A37829 | parasporal crystal |

| | | | | | |
|-----|-------|------|------|----------|--------------------|
| 30 | 867.5 | 25.5 | 1177 | 2 A49785 | parasporal crystal |
| 31 | 867 | 25.5 | 1178 | 1 USBSKH | parasporal crystal |
| 32 | 866.5 | 25.4 | 1166 | 2 S32645 | parasporal crystal |
| 33 | 866 | 25.4 | 1176 | 2 A22617 | parasporal crystal |
| 34 | 866 | 25.4 | 1176 | 2 S02215 | parasporal crystal |
| 35 | 861.5 | 25.3 | 618 | 2 S11445 | parasporal crystal |
| 36 | 845 | 24.8 | 1174 | 2 S32649 | parasporal crystal |
| 37 | 838.5 | 24.6 | 1165 | 2 S11446 | parasporal crystal |
| 38 | 828 | 24.3 | 1160 | 2 S32647 | parasporal crystal |
| 39 | 809 | 23.8 | 1156 | 2 A29838 | parasporal crystal |
| 40 | 787.5 | 23.1 | 1172 | 2 S32689 | parasporal crystal |
| 41 | 700 | 20.6 | 380 | 2 B42459 | parasporal crystal |
| 42 | 679 | 19.9 | 1156 | 2 S19306 | parasporal crystal |
| 43 | 665.5 | 19.5 | 934 | 2 B29838 | parasporal crystal |
| 44 | 656.5 | 19.3 | 1136 | 1 USBS81 | parasporal crystal |
| 45 | 637.5 | 18.7 | 1180 | 2 I39870 | parasporal crystal |
| 46 | 634.5 | 18.6 | 1180 | 2 A26858 | parasporal crystal |
| 47 | 482 | 14.2 | 613 | 2 JC6033 | parasporal crystal |
| 48 | 279.5 | 8.2 | 1245 | 2 T18211 | parasporal crystal |
| 49 | 245.5 | 7.2 | 633 | 2 C32053 | parasporal crystal |
| 50 | 245 | 7.2 | 633 | 2 D32053 | parasporal crystal |
| 51 | 236 | 6.9 | 1385 | 2 T18213 | parasporal crystal |
| 52 | 233 | 6.8 | 282 | 2 A25140 | parasporal crystal |
| 53 | 228.5 | 6.7 | 1289 | 2 T18212 | parasporal crystal |
| 54 | 228 | 6.7 | 622 | 2 S17402 | parasporal crystal |
| 55 | 219.5 | 6.4 | 643 | 2 A43647 | parasporal crystal |
| 56 | 215.5 | 6.3 | 1186 | 2 T18210 | parasporal crystal |
| 57 | 138 | 4.1 | 904 | 2 G90563 | parasporal crystal |
| 58 | 129.5 | 3.8 | 2139 | 2 S46404 | parasporal crystal |
| 59 | 127.5 | 3.7 | 1513 | 2 S45768 | parasporal crystal |
| 60 | 126 | 3.7 | 937 | 2 C97168 | parasporal crystal |
| 61 | 125.5 | 3.7 | 1193 | 2 S68218 | parasporal crystal |
| 62 | 124 | 3.6 | 753 | 2 AG1710 | parasporal crystal |
| 63 | 121.5 | 3.6 | 1138 | 2 A82939 | parasporal crystal |
| 64 | 121.5 | 3.6 | 2529 | 2 B64635 | parasporal crystal |
| 65 | 120.5 | 3.5 | 1193 | 2 JC4901 | parasporal crystal |
| 66 | 120 | 3.5 | 545 | 2 F86834 | parasporal crystal |
| 67 | 119.5 | 3.5 | 835 | 2 E72305 | parasporal crystal |
| 68 | 119.5 | 3.5 | 1946 | 2 EC6032 | parasporal crystal |
| 69 | 119 | 3.5 | 773 | 2 JE0387 | parasporal crystal |
| 70 | 119 | 3.5 | 1474 | 2 T18281 | parasporal crystal |
| 71 | 118 | 3.5 | 1127 | 2 T28317 | parasporal crystal |
| 72 | 118 | 3.5 | 1285 | 2 S70582 | parasporal crystal |
| 73 | 118 | 3.5 | 2166 | 2 G70163 | parasporal crystal |
| 74 | 117.5 | 3.4 | 753 | 2 A11339 | parasporal crystal |
| 75 | 117.5 | 3.4 | 2399 | 2 H71879 | parasporal crystal |
| 76 | 117.5 | 3.4 | 4688 | 2 F82885 | parasporal crystal |
| 77 | 117 | 3.4 | 1175 | 2 F64489 | parasporal crystal |
| 78 | 117 | 3.4 | 2334 | 2 S32920 | parasporal crystal |
| 79 | 116.5 | 3.4 | 767 | 2 F71479 | parasporal crystal |
| 80 | 116 | 3.4 | 804 | 2 A53211 | parasporal crystal |
| 81 | 115.5 | 3.4 | 1276 | 2 S11455 | parasporal crystal |
| 82 | 115 | 3.4 | 770 | 2 A11769 | parasporal crystal |
| 83 | 115 | 3.4 | 802 | 2 A29317 | parasporal crystal |
| 84 | 114.5 | 3.4 | 376 | 2 A90206 | parasporal crystal |
| 85 | 114.5 | 3.4 | 863 | 2 G96964 | parasporal crystal |
| 86 | 114.5 | 3.4 | 1193 | 2 G71605 | parasporal crystal |
| 87 | 114.5 | 3.4 | 1516 | 2 E71619 | parasporal crystal |
| 88 | 114 | 3.3 | 713 | 1 ALBSG1 | parasporal crystal |
| 89 | 114 | 3.3 | 803 | 2 A35954 | parasporal crystal |
| 90 | 114 | 3.3 | 925 | 2 D59105 | parasporal crystal |
| 91 | 114 | 3.3 | 1118 | 2 T28426 | parasporal crystal |
| 92 | 114 | 3.3 | 1407 | 2 S59823 | parasporal crystal |
| 93 | 114 | 3.3 | 2244 | 2 F90563 | parasporal crystal |
| 94 | 113.5 | 3.3 | 547 | 2 G69620 | parasporal crystal |
| 95 | 113.5 | 3.3 | 1806 | 2 AF1717 | parasporal crystal |
| 96 | 113 | 3.3 | 644 | 2 T21137 | parasporal crystal |
| 97 | 113 | 3.3 | 749 | 2 T31536 | parasporal crystal |
| 98 | 113 | 3.3 | 1209 | 2 AH2052 | parasporal crystal |
| 99 | 113 | 3.3 | 1477 | 2 T18534 | parasporal crystal |
| 100 | 112.5 | 3.3 | 566 | 2 T50382 | parasporal crystal |
| 101 | 112.5 | 3.3 | 2401 | 2 T28676 | parasporal crystal |
| 102 | 112 | 3.3 | 1375 | 2 S48375 | parasporal crystal |

| | | | | | |
|-----|-------|-----|------|---|--------|
| 103 | 111 | 3.3 | 1017 | 2 | T18488 |
| 104 | 111 | 3.3 | 1067 | 2 | T28663 |
| 105 | 111 | 3.3 | 1658 | 2 | S55101 |
| 106 | 111 | 3.3 | 2910 | 2 | T28156 |
| 107 | 110.5 | 3.2 | 520 | 2 | T18124 |
| 108 | 110.5 | 3.2 | 2485 | 1 | H71621 |
| 109 | 110 | 3.2 | 725 | 2 | T19994 |
| 110 | 110 | 3.2 | 814 | 1 | C40618 |
| 111 | 110 | 3.2 | 1616 | 2 | T16600 |
| 112 | 109.5 | 3.2 | 957 | 2 | H97800 |
| 113 | 109.5 | 3.2 | 986 | 2 | E90596 |
| 114 | 109.5 | 3.2 | 1103 | 2 | H82884 |
| 115 | 109.5 | 3.2 | 1119 | 2 | B70126 |
| 116 | 109 | 3.2 | 726 | 2 | S62180 |
| 117 | 109 | 3.2 | 804 | 2 | S51358 |
| 118 | 109 | 3.2 | 1202 | 1 | S05362 |
| 119 | 109 | 3.2 | 2819 | 2 | A90551 |
| 120 | 108.5 | 3.2 | 540 | 2 | T03754 |
| 121 | 108.5 | 3.2 | 775 | 1 | VPXRW6 |
| 122 | 108.5 | 3.2 | 4450 | 2 | FX0340 |
| 123 | 108.5 | 3.2 | 4550 | 2 | T18440 |
| 124 | 108 | 3.2 | 593 | 2 | F64523 |
| 125 | 108 | 3.2 | 851 | 2 | S50670 |
| 126 | 108 | 3.2 | 986 | 2 | H90565 |
| 127 | 107.5 | 3.2 | 1086 | 2 | T43266 |
| 128 | 107.5 | 3.2 | 1086 | 2 | T02442 |
| 129 | 107.5 | 3.2 | 1468 | 1 | S30818 |
| 130 | 107.5 | 3.2 | 1790 | 1 | S27772 |
| 131 | 107 | 3.1 | 300 | 2 | T08453 |
| 132 | 107 | 3.1 | 1048 | 2 | H64459 |
| 133 | 107 | 3.1 | 1599 | 2 | S22737 |
| 134 | 107 | 3.1 | 2178 | 2 | S55805 |
| 135 | 107 | 3.1 | 2364 | 2 | T40884 |
| 136 | 107 | 3.1 | 3262 | 2 | AH2137 |
| 137 | 107 | 3.1 | 4196 | 2 | T43274 |
| 138 | 106.5 | 3.1 | 822 | 2 | AB2507 |
| 139 | 106.5 | 3.1 | 834 | 2 | B82940 |
| 140 | 106.5 | 3.1 | 891 | 2 | G89957 |
| 141 | 106.5 | 3.1 | 945 | 2 | A64714 |
| 142 | 106.5 | 3.1 | 1272 | 2 | S60999 |
| 143 | 106.5 | 3.1 | 1279 | 2 | E64709 |
| 144 | 106.5 | 3.1 | 1959 | 2 | AG1085 |
| 145 | 106.5 | 3.1 | 4563 | 1 | LPH0UB |
| 146 | 106 | 3.1 | 483 | 2 | E70363 |
| 147 | 106 | 3.1 | 659 | 1 | A64228 |
| 148 | 106 | 3.1 | 1291 | 1 | A49777 |
| 149 | 106 | 3.1 | 1291 | 2 | S46431 |
| 150 | 106 | 3.1 | 2077 | 2 | T44178 |

ALIGNMENTS

RESULT 1
I39811
parasporal crystal protein cry3Bb1 - *Bacillus thuringiensis*
N;Alternate names: parasporal crystal protein cryIIIB2
C;Species: *Bacillus thuringiensis*
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: I39811
R;Donovan, W.P.; Rupaar, M.J.; Slaney, A.C.; Malvar, T.; Gawron-Burks, M.C.; Johnson, T.H.
Appl. Environ. Microbiol. 58, 3921-3927, 1992
A;Title: Characterization of two genes encoding *Bacillus thuringiensis* insecticidal crystals
A;Reference number: I39811; MUID:93119147; PMID:1476436
A;Accession: I39811
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-652 <RES>
A;Cross-references: UNIPROT:Q06117; GB:M89794; NID:G142729; PIDN:AAA22334.1; PID:G142730
C;Genetics:
C;Superfamily: parasporal crystal protein
C;Gene: cryIIIB2

| | Query Match | 100.0%; | Score 3406; | DB 2; | Length 652; |
|----|-----------------------|--|---------------------|-----------|-------------|
| | Best Local Similarity | 100.0%; | Pred. No. 3.1e-210; | | |
| | Matches 652; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| Qy | 1 | MNPNNRSEHDTIKVTNPSEIQTNHNQYPLADNPSTLEELNKFELRMTEDSSTEVL | DNS 60 | | |
| Db | 1 | MNPNNRSEHDTIKVTNPSEIQTNHNQYPLADNPSTLEELNKFELRMTEDSSTEVL | DNS 60 | | |
| Qy | 61 | TVKDAVGTGISVVGQILGVGVPPFAGALTSFYQSFLNTIWPSSDADPWKAPMAQVEVL | IDK 120 | | |
| Db | 61 | TVKDAVGTGISVVGQILGVGVPPFAGALTSFYQSFLNTIWPSSDADPWKAPMAQVEVL | IDK 120 | | |
| Qy | 121 | KIEEYAKSKALAELOGLQNNFEDYVNALNSWKKTPLSLRSKRQSDRIRELFSQAESHFRN | 180 | | |
| Db | 121 | KIEEYAKSKALAELOGLQNNFEDYVNALNSWKKTPLSLRSKRQSDRIRELFSQAESHFRN | 180 | | |
| Qy | 181 | SMPSFAVSKPEVLFLEPTYAQAAANTHLLLLKDAQVFGEEWGYSSDEVAEFYHRQIKLTQOY | 240 | | |
| Db | 181 | SMPSFAVSKPEVLFLEPTYAQAAANTHLLLLKDAQVFGEEWGYSSDEVAEFYHRQIKLTQOY | 240 | | |
| Qy | 241 | TDHCNVNWNGLNGLRGSTVDAMVKFNRRPREMTLTVLDLIVLPPFYDILRYLSKGVKTEL | 300 | | |
| Db | 241 | TDHCNVNWNGLNGLRGSTVDAMVKFNRRPREMTLTVLDLIVLPPFYDILRYLSKGVKTEL | 300 | | |
| Qy | 301 | TRDIFTDPIFSLNTLOEYGTPTFLSIENSIRKPHLFDYLOGIEPHTRLOPGYFGKDSFNWY | 360 | | |
| Db | 301 | TRDIFTDPIFSLNTLOEYGTPTFLSIENSIRKPHLFDYLOGIEPHTRLOPGYFGKDSFNWY | 360 | | |
| Qy | 361 | SGNYVETRPSIGSKKTIITSPFYGDKSTEPVOKLSFDGQKVYRTIANTDVAAPNGKVYLG | 420 | | |
| Db | 361 | SGNYVETRPSIGSKKTIITSPFYGDKSTEPVOKLSFDGQKVYRTIANTDVAAPNGKVYLG | 420 | | |
| Qy | 421 | VTKVDFSQYDDQKNETSTQYDSCRNNGHVSAQDSIDLQPPETTDEPLEKAYSHQLNAYE | 480 | | |
| Db | 421 | VTKVDFSQYDDQKNETSTQYDSCRNNGHVSAQDSIDLQPPETTDEPLEKAYSHQLNAYE | 480 | | |
| Qy | 481 | CFLMQDRRGITIPFTTWTHRSVDFFNTIDAEBKIKTQLPVVKAYALSSGASIIIEGPGFTCGNL | 540 | | |
| Db | 481 | CFLMQDRRGITIPFTTWTHRSVDFFNTIDAEBKIKTQLPVVKAYALSSGASIIIEGPGFTCGNL | 540 | | |
| Qy | 541 | LFLKESSENSIAKPKVTLNSAALLQRYRVRIRYASTTNLRLFVQNSNDDFLVIYINKTMWK | 600 | | |
| Db | 541 | LFLKESSENSIAKPKVTLNSAALLQRYRVRIRYASTTNLRLFVQNSNDDFLVIYINKTMWK | 600 | | |
| Qy | 601 | DDDLTYQTFDLATNSNMGPSGDKNELIIIGAESFVSNEKIIYIDKIEFIPVOL | 652 | | |
| Db | 601 | DDDLTYQTFDLATNSNMGPSGDKNELIIIGAESFVSNEKIIYIDKIEFIPVOL | 652 | | |

RESULT 2

S10228
 Parasporeal crystal protein cry3Ba1 - *Bacillus thuringiensis* (fragment)
 N:Alternate names: coleopteran-active parasporeal crystal protein; delta-endotoxin
 C:Species: *Bacillus thuringiensis*
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C:Accession: S10228
 R:Sick, A.; Gaertner, F.; Wong, A.
 Nucleic Acids Res. 18, 1305, 1990
 A>Title: Nucleotide sequence of a coleopteran-active toxin gene from a new isolate of *Bacillus thuringiensis*
 A:Reference number: S10228; MUID:90206811; PMID:3220431
 A:Accession: S10228
 A>Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-659 <SIC>
 A:Cross-references: UNIPROT:P17969; EMBL:X17123; NID:g40258; PIDN:CAA34983.1; PID:g40259
 C:Genetics:
 A:Gene: cryIIIB
 C:Superfamily: parasporeal crystal protein
 C:Keywords: delta-endotoxin; toxin

| | | | | |
|-----------------------|------------------|---------------------|-----------|-------------|
| Query Match | 94.3% | Score 3212; | DB 2; | Length 659; |
| Best Local Similarity | 93.7%; | Pred. No. 8.2e-198; | | |
| Matches 610. | Conservative 22; | Mismatches 19; | Indels 0; | Gaps 0; |

301 TRDIPTDPIFSLNTLOEYGTPTFLSIENSIRKPHLDYLOGIEBFHTRLOFGYFGKDSFNW 360
 298 TRDVLTPDPIVAVNNMNGYGTTFSTNENIRKPHLDYLOHAFHSLRLOQGYGTDSFNW 357
 361 SGNVETRPSIGSSKTIITSPFYGDKSTPEVQKLSFDGQKVYRTIANTDVAAPNG---K 416
 358 SGNVSTRSIGSDIIRSPFYGNKSTLDVQNFENGEKVFRAVANGNLAVPVGTTGK 417
 417 VILGVTKVDSQVDDOKNETSTQTYDSKNNGHVSAQDSIDQLPPTTDEPLEKAYSHQL 476
 418 IHSVTKVDFSOYNDKRDVTRQTYDSKNNVGGI-VFDSIDQLPPTTDEPLEKAYSHQL 476
 477 NYAECLFMDDRRGTIPFFTWTHRSVDFNTIDAEKITQLPVVKAYALSSGASIEGPPT 536
 477 NYVRCFLQGRGLIIPVFTWTHKSVDFNTLDSEKITQIPFVKAFILVNSTSVAGPPT 536
 537 GGNLLFLKSSNSIAKPKVTLSAALLQRYVRIRVASTTNLRLFVQNSNNDPLVIYINK 596
 537 GGDIIKCTNGS-GLTLYVTPAPDLTYSKYKIRYASTSQVRFGIDLGSYTHSISYFDK 595
 597 TMKDDDLTYQTDLATTNSMFGSGDKNELIIGAESFVSNKEIYIDKIEFIPV 650
 596 TMDKNTLTYSNPLNSVSRPIEISG-NKIGSVGGISGDEVDYIDKIEFIPM 648

RESULT 5
 S49247
 paraaporal crystal protein cry9Cal [validated] - Bacillus thuringiensis
 N:Alternate names: paraaporal crystal protein cryIH
 C:Species: Bacillus thuringiensis
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C:Accession: A59350; S49247
 R:Lambert, B.; Buyse, L.; Decock, C.; Jansens, S.; Piens, C.; Saey, B.; Seurinck, J.; V
 Appl. Environ. Microbiol. 62, 80-86, 1996
 A:Title: A Bacillus thuringiensis insecticidal crystal protein with a high activity agair
 A:Reference number: A59350; MUID:96141404; PMID:8527215
 A:Accession: A59350
 A:Molecule type: DNA
 A:Residues: 1-1157 <LAM>
 A:Cross-references: UNIPROT:Q45733; EMBL:Z37527; NID:G547554; PIDN:CAA85764.1; PID:G5475
 A:Experimental source: serovar tolworthi
 C:Comment: This paraaporal crystal protein, active against corn borer and other insects,
 C:Superfamily: paraaporal crystal protein
 C:Keywords: delta-endotoxin

Query Match 33.1%; Score 1127.5; DB 1; Length 1157;
 Best Local Similarity 36.1%; Pred. No. 4.8e-64;
 Matches 250; Conservative 148; Mismatches 217; Indels 77; Gaps 19;

QY 1 MNPNNRSEHDTIKVTPNSELOTNNH-QYPLADNPSTLEELNYKEFLMTEDSDSTEVLN 59
 DB 1 MNRNNQNEVEIID-APHGCGPDDDDRYPLASDPNAAALQNNYKDYLOMTDEDYDYSIN 59
 QY 60 STV---KDAVGTGIVSVGQIILGVVVPFAGALTSFYQSFLNTIWP-SDADPWKAFMAQV 114
 DB 60 PSLISGRDAVQATLTVVGRILGALGVPSQIGVSYFQFLNTLWPNVDLTAWEAFMQV 119
 QY 115 EVLIDKIEYAKSALAELOQLNNFEDYVNALNSWKKTPLSLRS-KRSQRIEFLFSQ 173
 DB 120 EELVNCQITEFARNQALRLQGLGDSFNQYQSLQNW---LADNDRNLNSVVAQFIA 175
 QY 174 ASHFNRNMPSTAVSKFEVLFLPTTAAQANTHLLKDAQVFGEBWGSSEDAEYFHRQ 233
 DB 176 LBLDFVNAIPLFAVNGQQVPLLSVVAQVNLHLLKDALEFGEWGTQGEISYIDRQ 235
 QY 234 LKLTQOYTDHCVNNGVNLGLRGSTYDAWKFNFRREMTLTVDLIVLFFPYDIRLYS 293
 DB 236 LELTAKYTNVCEWYNTGLDRLGNTESWLRHYHQFRREMTLVLDVVAALFPYDVRLYP 295
 QY 294 KGKTELTDRDIFDTPF-----SLNTLOEYGP-----TFLSIENS-IRKPHLDYLOGIEBF 343
 DB 296 TGSNPQLTREVTDPITVFVNPANVGLCRWGTNPNYTFSELENAFIRPPLHFDRLNLSLI 355

241 TDHCYNNVNGLNGRSGTSDAWKFNFRREMTLTVDLIVLFFPYDIRLYSGVKTEL 300
 248 TDHCYNNVNGLNGRSGTSDAWKFNFRREMTLTVDLIVLFFPYDIRLYSGVKTEL 307
 301 TRDIPTDPIFSLNTLOEYGTPTFLSIENSIRKPHLDYLOGIEBFHTRLOFGYFGKDSFNW 360
 308 TRDVLTPDPIVAVNNMNGYGTTFSTNENIRKPHLDYLOHAFHSLRLOQGYGTDSFNW 357
 361 SGNVETRPSIGSSKTIITSPFYGDKSTPEVQKLSFDGQKVYRTIANTDVAAPNGKVVYLG 420
 368 SGNVSTRSIGSDIIRSPFYGNKSTLDVQNFENGEKVFRAVANGNLAVPVGTTGK 417
 417 VILGVTKVDSQVDDOKNETSTQTYDSKNNGHVSAQDSIDQLPPTTDEPLEKAYSHQLNAE 480
 427 VTKVPSQNDQDDEASTQTYDSKNNVGGI-WDSIDQLPPTTDEPLEKAYSHQLNVM 485
 481 CFLMQDRRGTIPFFTWTHRSVDFNTIDAEKITQLPVVKAYALSSGASIEGPPTGNNL 540
 486 CFLMQSGRTIPVLTWTHKSVDFNTIDAEKITQLPVVKAYALSSGASVAGPPTGDI 545
 541 LFLKSSNSIAKPKVTLSAALLQRYVRIRVASTTNLRLFVQNSNNDPLVIYINKTMK 600
 546 IQCTE-NGSAATYVT-PDVVSQKTRARIHASTSQVTFILSLDGAEPNQYFPKTIK 603
 601 DDLTYQTDLATTNSMFGSGDKNELIIGAESFVSNKEIYIDKIEFIPV 650
 604 GDTLTYSNPLNSVSRPIEISG--NNLQIGVTGLSAGDKVYIDKIEFIPV 651

RESULT 4
 JH0261
 paraaporal crystal protein cry3Cal - Bacillus thuringiensis subsp. kurstaki (strain BT11
 N:Alternate names: paraaporal crystal protein cryIIID
 C:Species: Bacillus thuringiensis subsp. kurstaki
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: JH0261; S18944
 R:Lambert, B.; Theunis, W.; Aguda, R.; Van Audenhove, K.; Decock, C.; Jansens, S.; Seuri
 Gene 110, 131-132, 1992
 A:Title: Nucleotide sequence of gene cryIIID encoding a novel coleopteran-active crystal
 A:Reference number: JH0261; MUID:92184108; PMID:1544571
 A:Accession: JH0261
 A:Molecule type: DNA
 A:Residues: 1-649 <LAM>
 A:Cross-references: UNIPROT:Q45744; EMBL:X59797; NID:G40287; PIDN:CAA42469.1; PID:G40288
 A:Genetics:
 C:Gene: cryIIID
 C:Superfamily: paraaporal crystal protein

Query Match 63.2%; Score 2152; DB 1; Length 649;
 Best Local Similarity 62.2%; Pred. No. 5.6e-130;
 Matches 407; Conservative 95; Mismatches 142; Indels 10; Gaps 6;

QY 1 MNPNNRSEHDTIKVTPNSELOTNNH-QYPLADNPSTLEELNYKEFLMTEDSDSTEVLN 59
 DB 1 MNRNNQNEVEIID-APHGCGPDDDDRYPLASDPNAAALQNNYKDYLOMTDEDYDYSIN 59
 QY 61 TVKDAVGTGIVSVGQIILGVVVPFAGALTSFYQSFLNTIWP-SDADPWKAFMAQV 114
 DB 59 TTKDAIQKGIIGLLGVGFPYGGALVSFYTNLLNTIWPGE-DPLKAFMQVEALIDQ 117
 QY 121 KIEEYAKSALAELOQLNNFEDYVNALNSWKKTPLSLRS-KRSQRIEFLFSQAEHFRN 180
 DB 118 KIADYAKDAKAELOQLKNNFQDYVSLDSWDKPTLTDGSSQGRIRLFSQAEHFR 177
 QY 181 SMPSPAVSKFEVLFLPTTAAQANTHLLKDAQVFGEBWGSSEDAEYFHRQLKTOY 240
 DB 178 SMPSPAVSGEYVFLPTTAAQANTHLLKDAQVFGEBWGSSEDAEYFHRQLKTOY 237
 QY 241 TDHCYNNVNGLNGRSGTSDAWKFNFRREMTLTVDLIVLFFPYDIRLYSGVKTEL 300
 DB 238 TNHCAKRYKAGLDKLRGTYEAWKFNFRREMTLTVDLIVLFFPYDIRLYSGVKTEL 297

| | | | | |
|----|---|-----|--|---------------|
| QY | | 343 | PHTLQPGYFGKDSFNWGNVVERPSPISIGSSKITITSPFYGDKSTEPVQKLSPDGQKVYR | 402 |
| Db | : | 344 | IYSLLS-RWNTOYMNMGHKKLEFR-TIGGTNLISTQGSTNTSINPV-TLPFTSRDVR | 400 |
| QY | : | 403 | TIANTDVAAMPNGKVKYLGVTKVDFSDYDDQKNETSTQTYDSKRNGH---- | VSQAQSDIQ 458 |
| Db | : | 401 | TESLAGLNLFITQPN-VPRVDF-----HWKFVTPIASDNFFYPGYAGICTQLODSENE | 455 |
| QY | : | 459 | LPPETTEDEPLEKAYSHOLNVAECFLMQDRRGITPFPTWTHRSVDFFNITDAEKITQLPW | 518 |
| Db | : | 456 | LPEATGQPNYESYSHLSHGIIASHVKALV-:YSWTHRSADRTNIENSIQTPLV | 513 |
| QY | : | 519 | KAYALLSSGASTIEGPFTGGNLLFLKESNSIAKFKVTLNSAALLQRYVRIRYASTTNL | 578 |
| Db | : | 514 | KAFNLLSGAAVVRRPGFTGGILL-RTNTGTFGDIRVNIN-PPEAQRYVRIRYASTTDL | 571 |
| QY | : | 579 | RLEVQ-----NSNNDELVIYINKNMKODDLTYQTFDLATNNSMNGFSGDKNELLIGAE | 632 |
| Db | : | 572 | QPHTSINGAKAINQGN-----PSATMURGEDLDKYTFRTVGTTFPFSLDVQOSTFTIGAW | 625 |
| QY | : | 633 | SFVSNKEIYIDKBIFIPVOL | 652 |
| Db | : | 626 | NFESSGNEVVIDRIEFPVEV | 645 |

I39814
insecticidal protein cryv1 - *Bacillus thuringiensis*
C/Species: *Bacillus thuringiensis*
C/Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999
C/Accession: I39814
R/Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61, 2402-2407, 1995
A/Title: Distribution of cryv-type insecticidal protein genes in *Bacillus thuringiensis*
tomocidus.
A/Reference number: I39814; MUID:95314293; PMID:7793960
A/Accession: I39814
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-719 <RES>
A/Cross-references: GB:I36338; NID:g540281; PIDN:AAC36999.1; PID:g540282
C/Genetics:
A/Gene: cryv1
C/Superfamily: parasporal crystal protein

[illegible]


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QY 343 FHTRLQPGYFKDSEFNWGSNYVETRPSIGSSKTIITSPFYGDKSTEPVQKLSFDGOKVYR 402
Db 344 IYSLLS-RWNTQYMNWGMGHKLEFR-TIGTLNISTQGSTNTSINPV-TLPFTSRDVIYR 400
QY 403 TIANTDVAAMPNGKVYLGVTQKDFPSQYDDQKNETSTQTYDSKRNNGH-----VSAQDSIDQ 458
Db 401 TESLAGLNLFLTPQVNV-GVPRVDF-----HWKFVTHPIASDNFYYPGVAGIGTQLQDSENE 455
QY 459 LPPEITDEPLEKAYSHOLNVAECFLMQDRRGITPFFFTWTHRSVDFNTDAEKITQLPVV 518
Db 456 LPEATGQPNYESYSHLSHIGLISASHVKALV--YSWTHRSADRTNTIEPNSITQPLV 513
QY 519 KAYALSSGASIIIGPGFTGGNLLFLKESNSIAKFVKTLNSAALLQRYRIRIYASTTNL 578
Db 514 KAFNLSSGAAVRGPFGTGGDIL-RRNTGTFGDIRVIN-PPFAQRYRIRIYASTTDL 571
QY 579 RLFPVQ-----NSNNDPLVIYINKTMKODDLTYQTDFLATTNMGMFSGDKNELIIGAE 632
Db 572 QFHTSINGKAINQGN-----FSATMNRGSDLDYKTRTVGFTTTPFSFLDVQSTFTIGAW 625
QY 633 SFVSNKIIYDKIEFIPVQL 652
Db 626 NFSSGNEVIYDRIEFVPEV 645

RESULT 10
S25383
paraesporal crystal protein cryllal - Bacillus thuringiensis
N;Alternate names: delta-endotoxin; paraesporal crystal protein cryv
C;Species: Bacillus thuringiensis
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S25383
R;Tailor, R.; Tippett, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.
Mol. Microbiol. 6, 1211-1217, 1992
A;Title: Identification and characterization of a novel Bacillus thuringiensis delta-end
A;Reference number: S25383; MUID:92269582; PMID:1588820
A;Accession: S25383
A;Molecule type: DNA
A;Residues: 1-719 <TAI>
A;Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:g40289; PIDN:CAA44633.1; PID:g40290
C;Genetics:
A;Gene: cryv
C;Superfamily: paraesporal crystal protein
C;Keywords: delta-endotoxin

Query Match 32.0%; Score 1091.5; DB 2; Length 719;
Best Local Similarity 36.5%; Pred. No. 4.9e-62;
Matches 248; Conservative 137; Mismatches 232; Indels 63; Gaps 19;

QY 1 MNPNNRSEHDTI-----KVTNSELQTNHNOYPLADNPNSLLELNKYKEFLRMTESS 53
Db 1 MKLNQDKQSFSSNAKVDKISTDS-----LNKETDIELQNHEDCLMKSEYEN 50
QY 54 TE-VLDNSTKDAVGTGIVGVGQILGVVGPFGALTSFYQSFLNTIWPSSDADPWKAFMA 112
Db 51 VEPFVASTIQ----TGIGIAGKILGTGLVPPAGQVASYLSFILGELMPKGNQWEIFME 106
QY 113 QVEVLDDKIEEYAKSALAELOGLQNNFEDYVNALNSKKTPLSLRKSRQDRIRBELFS 172
Db 107 HVEEIIQKISTYARNKALTDLKGLDALAVYHDSLESVWG---NNNTRARSVKSQYI 163
QY 173 QAESHERNSMPSFAVSKFEVLFLPTVAQAANTHLLLLKDAQVGEWGSYSSDEVAEFYHR 232
Db 164 ALELMFVQKLPSFAVSGEEVPLPIYQAANLHLLLRDASIFGKEWGLSSSEISTFYNR 223
QY 233 QLKLTQQYTDHCVNWNVGLNGURGSTYDAWVKFNFRREMTLTVLVDLIVLFFPYDIRLY 292
Db 224 OVERAGDYSVHCVKMTSTGLNLRGTAESWVRYNQFRDMLTLVLDLVALPFSYDTQY 283
QY 293 SGKVKTELTRDITD-----PIFLNT-LOEYGPFTLSIENS-IRKPHLFDYLOGIE 342
Db 284 PIKTTAQLTREYVTAIGTVHHPHSFTSTTWNNNAPSFSAEAAVVRNPHLLIDLEQVT 343
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QY 343 FHTRLQPGYFKDSEFNWGSNYVETRPSIGSSKTIITSPFYGDKSTEPVQKLSFDGOKVYR 402
Db 344 IYSLLS-RWNTQYMNWGMGHKLEFR-TIGTLNISTQGSTNTSINPV-TLPFTSRDVIYR 400
QY 403 TIANTDVAAMPNGKVYLGVTQKDFPSQYDDQKNETSTQTYDSKRNNGH-----VSAQDSIDQ 458
Db 401 TESLAGLNLFLTPQVNV-GVPRVDF-----HWKFVTHPIASDNFYYPGVAGIGTQLQDSENE 455
QY 459 LPPEITDEPLEKAYSHOLNVAECFLMQDRRGITPFFFTWTHRSVDFNTDAEKITQLPVV 518
Db 456 LPEATGQPNYESYSHLSHIGLISASHVKALV--YSWTHRSADRTNTIEPNSITQPLV 513
QY 519 KAYALSSGASIIIGPGFTGGNLLFLKESNSIAKFVKTLNSAALLQRYRIRIYASTTNL 578
Db 514 KAFNLSSGAAVRGPFGTGGDIL-RRNTGTFGDIRVIN-PPFAQRYRIRIYASTTDL 571
QY 579 RLFPVQ-----NSNNDPLVIYINKTMKODDLTYQTDFLATTNMGMFSGDKNELIIGAE 632
Db 572 QFHTSINGKAINQGN-----FSATMNRGSDLDYKTRTVGFTTTPFSFLDVQSTFTIGAW 625
QY 633 SFVSNKIIYDKIEFIPVQL 652
Db 626 NFSSGNEVIYDRIEFVPEV 645

RESULT 11
S00873
paraesporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis
N;Alternate names: paraesporal crystal protein cryA4
C;Species: Bacillus thuringiensis subsp. thuringiensis
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S00873
R;Brizzard, B.L.; Whiteley, H.R.
Nucleic Acids Res. 16, 2733-2724, 1988
A;Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus t
A;Reference number: S00873; MUID:88203216; PMID:3362680
A;Accession: S00873
A;Molecule type: DNA
A;Residues: 1-1228 <BRI>
A;Cross-references: UNIPROT:P05517; EMBL:X06711; NID:g40264; PIDN:CAA39898.1; PID:g58094;
C;Genetics:
A;Gene: cryA4
A;Start codon: TTG
C;Superfamily: paraesporal crystal protein
C;Keywords: delta-endotoxin

Query Match 31.5%; Score 1072.5; DB 2; Length 1228;
Best Local Similarity 36.6%; Pred. No. 1.7e-60;
Matches 246; Conservative 120; Mismatches 247; Indels 59; Gaps 19;

QY 1 MNPNNRSEHDTIKVTNSELQTNHNOYPLADNPNSLLELNKYKEFLRMTESSSTEVLDNS 60
Db 1 MTSNRKNENEIINAVNSHSAQMD-----LLPDARIEDSLCIAEGNN---IDPF 45
QY 61 TVKDVAVGTGIVGVGQILGVVGPFGALTSFYQSFLNTIWPSSDADPWKAFMAQVEVLIDK 120
Db 46 VSASTVQTGINTAGRILGVIGVPPAGQLASFTSFLVGLWPRGRDQWELFLEHVEQLNQ 105
QY 121 KIEEYAKSALAELOGLQNNFEDYVNALNSKKTPLSLRKSRQDRIRE-LFSQ---AES 176
Db 106 QITENARNLTALRLQGLGSPRAYQGSLEWLE-----NRDDARTSRVLYTYQIALEL 158
QY 177 HFRNSMPSFAVSKFEVLFLPTVAQAANTHLLLLKDAQVGEWGSYSSDEVAEYHRLQKL 236
Db 159 DFLNAMPLFAIRNQSEVPLLMVYAQAANLHLLLRDASLFGSFGSLTSQSIQRYRQVER 218
QY 237 TQOYTQYTDHCVNWNVGLNGURGSTYDAWVKFNFRREMTLTVLVDLIVLFFPYDIRLSKGV 296
Db 219 TRDYSDYCVETWNTGLNSLRGTNAASWRYNQFRDMLTLGLVDLVALPFSYDTRTPINT 278
QY 297 KTELTRDITDPI-----FSLNTLQBYGPTFLSIE-NSIRKPHLFDYLOGIEFTRLQ 348
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Db 279 SAQLTREVVYDAIGATGVNMAWMNNYNNAPSFAIEAAAIRSPHLLDFLEQLTIFS-AS 337
Qy 349 POYFGKDSFNWNGYVETRPISGSKTITSPFYG--DKSTPEYQKLSFDGQKYYRIIAN 406
Db 338 SWSNTRHMYWRGHTISRPITGGGLNST--HGATNTSINPV-TLFPASRDYRTESY 393
Qy 407 TDVAAPNGKVYL----GVTKVDFQYDDQK-NETSTQYDSKRNGHVSQAQSDIDQLPP 461
Db 394 AGVLW--GIVLEPIHGVPVTRFNTPNQISDRGTANYSQPYESPGQLQKDSLETLP 450
Qy 462 ETTDPELEKAYSHQNLNACFLMQDRRTGTPPFTWTHRSVDFNTIDAEKITQLPVKAY 521
Db 451 ETTERPNYESYHRLSHIGIILQ--RVNVPYVSWTHRSADRTNTPGNRITQIPMWKAS 508
Qy 522 ALSSGASIEEGPFTGGNLLFLKESNSIAKPKVTLNSAALLQRYRVRIRVASTTNRLF 581
Db 509 ELPOGFTVVRGPGFTGGDIL-RTWGGPGPRVTNV-GPLTORVIRGFRVASTVDPDF 566
Qy 582 VQNSN---NDFLVIVYINKTMKDDDLTYOTFDLATNNSMGSGDKNELIIGAESFVUNE 638
Db 567 VSRGGTTVNVFRFL---RTMNGDELKYGNFVRRATPFTTQIQDIIRTSIQLSGNG 623
Qy 639 KIYIDKIEFIPV 650
Db 624 EYVIDKIEIIPV 635

RESULT 12
I40589
parasporal crystal protein cry8Cal - Bacillus thuringiensis
N;Alternate names: parasporal crystal protein cryIII
C;Species: Bacillus thuringiensis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40589
R;Sato,R.; Takeuchi, K.; Ogiwara, K.; Minami, M.; Kaji, Y.; Suzuki, N.; Hori, H.; Asano
Curt. Microbiol. 28, 15-19, 1994
A;Title: Cloning, heterologous expression, and localization of a novel crystal protein g
A;Reference number: I40589; MUID:94100786; PMID:7764305
A;Accession: I40589
A;Status: preliminary;
A;Molecule type: DNA
A;Residues: 1-1160 <RES>
A;Cross-references: UNIPROT:Q45706; EMBL:U04366; NID:g532523; PIDN:AAA21119.1; PID:g5325
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 31.1%; Score 1060; DB 2; Length 1160;
Best Local Similarity 37.1%; Pred. No. 1e-59;
Matches 254; Conservative 116; Mismatches 254; Indels 60; Gaps 21;

Qy 1 MNPNNRSEHTIKVTPNSELOTHNQYPLADNPNSTLEELNYKEFLMTEDSSTEVLDS 60
Db 1 MSPNNQNEYETIDALSPTSVDNSIRYPLANDQNTLQNNYKYDKLQMTSTNAELSRNP 60
Qy 61 ----TVKDAGTGISVVGQILGVGVVPFAGALTSFYQSFLNTIWP--DADPWKAFMAQVE 115
Db 61 GTFTISAQAVGTGIDIVSTTISGUGIPVLGEVFSILGSLGLMPNSNNVWQIFWNRVE 120
Qy 116 VLIDKIEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSURSKSQDRIRBELFSQAE 175
Db 121 ELIDQKILDSVRSRAIADLANSRITAVEYQNALEDWRKNP---HSTRSAALVKERFGNAE 177
Qy 176 SHFNSMPSFAVSKEFVLFLPTYAQAANTHLLKDAQVGEWGSSEVDAEFYHRQLK 235
Db 178 AILRTNMGFSQTNETPLPLPTYAQAASHLLVNRDQVIYKEGWYQNDIDILFYKEQVS 237
Qy 236 LTQOYTHCVNMYNGLNGRSTYDAWVKFNFRREMTLTVLDLIVLFPFYDIRLYSKG 295
Db 238 YTARYSDCHVQYVYAGNLKRGTKAKQWVDYNNFRRENNVWLDLVALFNFYDARIYPLE 297
Qy 296 VKTELTRDITDTPISLNTLQE-----YG-----PTFLSIENSIRKPHLFDVLQIEF 343
Db 298 TNAELTREIFTDPVGSYVVGQSSTLISWYDMIPALPFSFTLENLLRKRKPFDTLLQIRIM 357

Qy 344 HTRL-QPGYFGKDSFNWNGYVETRPISGSS-KTITSPPFYGDKSTPEYQKLSFDGQK-V 400
Db 358 YTSFRONGTI--EYNYWGGQRLTLGIYIYSSFNKYSGVLAGAEDIIPV-----QNDI 409
Qy 401 YRTIANTDVAAMWNGKVLGVTKVDFSQYDDQKNETSTQYDS-KRNGHVSQAQSDIDQL 459
Db 410 YRVW-TYGRYTN--LLGVNPTF-----YFSNNTQKTSKPKQFAGIKTIDSGEEL 461
Qy 460 PPETDPELEKAYSHQNLNACFLMQDRRTGTPPFTWTHRSVDFNTIDAEKITQL 515
Db 462 TYEN-----YQSYSHRVSYITTSPEIKSTGCTVLGVVPIFGWTHSSASRNNFYATKISQI 516
Qy 516 PVVKAYALSGA--SILEGPGFTGGNLLFLKESNSIAKPKVTLNSAALLQRYRVRIRYA 573
Db 517 PINKASRTSGAVNWFQEG-LYNGGPMVLSGSGSQVINLRVATDAKAGASQRYRIRYA 575
Qy 574 S-----TTNLRFLVQNSNNDFLVIVYINKTMKDDDLTYOTFDLATNNS-NMGFSGDKNE 626
Db 576 SDRAGKFTISSRSPENPATYSASIAVTN-TMSTNASLTSTPAYABSGPINLGISGSR 634
Qy 627 LIIGAESFVNEKIYIDKIEFIPV 650
Db 635 FDISITKEAGAANLYIDRIEFIPV 658

RESULT 13
S39536
parasporal crystal protein cry9Ba1 - Bacillus thuringiensis
N;Alternate names: Delta-endotoxin-related protein; parasporal crystal protein cryX
C;Species: Bacillus thuringiensis
C;Date: 07-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: S39536
R;Shevelev, A.B.; Svarinsk, M.A.; Karasin, A.I.; Kogan, Y.N.; Chestukhina, G.G.; Stepan
FBIS Lett. 336, 79-82, 1993
A;Title: Primary structure of the cryX, the novel delta-endotoxin-related gene from Bacil
A;Reference number: S39536; MUID:94085596; PMID:8262221
A;Accession: S39536
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1154 <SHE>
A;Cross-references: UNIPROT:Q45745; EMBL:X75019
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 28.3%; Score 963.5; DB 2; Length 1154;
Best Local Similarity 33.3%; Pred. No. 1.5e-53;
Matches 214; Conservative 135; Mismatches 243; Indels 51; Gaps 16;

Qy 41 NYKEFLRMT--DSSTEVLDNSTVDAGVTGTSVVGQILGVGVVPFAGALTSFYQSFLNTI 99
Db 29 SYKDYLKMSGDYIDSYINPGNVRTGLQTGIDIVAVVVGALGGPVGGILTGLFLTFLGFL 88
Qy 100 WPS-DADPWKAFMAQVEVLIDKIEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSL 158
Db 89 WPSNDQAAWEAPTEQIEELIEQISDQVVRALDLDLTGIONYYQYLYALKKEWERPNV 148
Qy 159 RSKRSQDRIRBELFSQAESHFRNSMPSPF----AVSKFEVLFLPTYAQAANTHLLKDAQV 214
Db 149 RA----NLVLQFEILHALFVSSMPSFGSGPQSRQFQAQLLVVYAQAANTHLLKDAQV 204
Qy 215 FGEWGYSSDVAEFYHRQLKL-TQOYTHCVNMYNGLNGRSTYDAWVKFNFRREM 273
Db 205 YGARWGLRESQNLGYFNELOTRTRDYNHCVNMYNGLNGRSTYDAWVKFNFRREM 264
Qy 274 TLTVLDLIVLFPFYDIRLYSKGKTELTTRDIFETDP-----IFSANTLQEVGP 320
Db 265 TLMADLLIALFYNTYTRRPIAVNPQLIREVTDPLVPSEBSSLFPELRLCRWQETSAM 324
Qy 321 TFLSIENS-IRKPHLFDYLOQIEFHTRLQPGYFGKDSFNWNGYVETRPISGSKTIFS 379
Db 325 TFSNLENALISSPHLPDITNNLMIVTGSFVSHLTNQLIEGWIGHSVTSLLASGPTTVLR 384

Db 390 EFS-----TPTNSFTY---RGRGTV---DSLTELPPEDNSVPPREGYSHRLCHA---TF 434
Qy 485 QDRRGTIPE-----FTWTHRSVDFNTIDAEEKITQLPFWKAYALSSGASIIIEGPGFTGG 538
Db 435 VQRSGT-PFLTGTGVFSWTHRSATLNTIDPERINQIPLVKGFRWGGTSVITGPGFTGG 493
Qy 539 NLLFLKSSNSIAKPKVTLSAALLQRYRVRIRYASTTNLRFLV-----QNSNN 587
Db 494 DIL-RRNTFGDFVSLQVINS-PITQRYRLRFRYASSRDARVILVTGAAGTGVGGQVSVN 551
Qy 588 DELVIYINKTKNDDLLTYOTFDLATTNSMGFS-----GDKNELIIGAESFVSNEKIY 641
Db 552 ----MPLQKTMEIGENLTSTFRYTFDSNPFSPRANPDIIIGISEQPLFGAGS-ISSGELY 606
Qy 642 IDKIEFI 648
Db 607 IDKIEII 613
RESULT 16
S04181
parasporal crystal protein - Bacillus thuringiensis (strain aizawai 7.29) (fragment)
N:Alternate names: delta-endotoxin
C:Species: Bacillus thuringiensis
C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: S04181
R:Sanchis, V.; Lereclus, D.; Menou, G.; Chaufaux, J.; Guo, S.; Lecadet, M.M.
Mol. Microbiol. 3, 229-238, 1989
A:Title: Nucleotide sequence and analysis of the N-terminal coding region of the Spodoptera frugiperda polyhedrin gene
A:Reference number: S04181, MUID:89343627, PMID:2548060
A:Accession: S04181
A:Molecule type: DNA
A:Residues: 1-823 <S>
A:Cross-references: UNIPROT:P05518; EMBL:X13620; NID:g40355; PIDN:CAA31951.1; PID:g40356
C:Genetics:
A:Gene: bta
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin
Query Match 26.4%; Score 907.5; DB 2; Length 823;
Best Local Similarity 35.8%; Pred. No. 3.5e-50;
Matches 239; Conservative 103; Mismatches 230; Indels 95; Gaps 27;
Qy 21 QTNHQ---YPLADNPSTLEELNYKEFLRMTESSTEVLDN---STVKDVGTVGISVVG 74
Db 3 ENNQNCIPYCNLSNPEEVL-----LDGERISTGSSIDISLSLV- 42
Qy 75 QILGVGVPPAGALTSFYQSFLNTIWPFSADPDKAFMAQVEVLIDKKIEYAKSKALAE 134
Db 43 QFLVSNFVPGGGLVGLIDFPVGVGSQ---WDAFLVQIEQLINERIAEFARNAAIANL 99
Qy 135 QGLQNPFDVYVYALNSWKKTPLSLRSKRSQDRIRLFSQAESHFRNSMPSFAVSKFVL 194
Db 100 EGLNNFNIEYAEKWEEDP---NNPATRVIDRFLDGLLLERDIPSFRTSGSEVPL 156
Qy 195 LPTVAQAAHTLLLDKDAQVFGREWGYSSEDAEFYHRLKLTQQYTDHCVNWNVYVGLNG 254
Db 157 LSVTAQAAHLALRLDSVIFGERWGLTTINVENYNLRIHIDEYADHCANYNGLAN 216
Qy 255 LRGSYDAWKFNRRREMTLVLDLVLVFPFYDIRLYSKGVKTELTDRIDTPIPSLN- 313
Db 217 LPKSTYQDWITYNRLRDLTLVLDIAAFFPNYDNRRYPIQPVGQLTREYTDPLINFNP 276
Qy 314 TLQBYG--PFLSLTENS-IRKPHLFDYLQIEFHRLQPCGVFGKDSFNWYSGNVYETRPS 370
Db 277 QLQSAVLPTFNWNSAIRNPHLFDILNLTPT-----DWFSVGRNFYWGHRVLS--S 330
Qy 371 IGSSKTTITSPYG-DKSTPEVQKLSFDGQKRYRT--IANTDVAAPNPKVYL---GVTKV 424
Db 331 LIGGNITSPYIGREANQEPFRSFTFG-PVFRTLSIPTLRLLQQPCORHHFNLRGEGV 389
Qy 425 DFGYDDQKNETSTQTVDSKRNNGHVSQAQSDIDQLPRTTDEPLEKAYSQLNVAECFLM 484

Db 390 EFS-----TPTNSFTY---RGRGTV---DSLTELPPEDNSVPPREGYSHRLCHA---TF 434
Qy 485 QDRRGTIPE-----FTWTHRSVDFNTIDAEEKITQLPFWKAYALSSGASIIIEGPGFTGG 538
Db 435 VQRSGT-PFLTGTGVFSWTHRSATLNTIDPERINQIPLVKGFRWGGTSVITGPGFTGG 493
Qy 539 NLLFLKSSNSIAKPKVTLSAALLQRYRVRIRYASTTNLRFLV-----QNSNN 587
Db 494 DIL-RRNTFGDFVSLQVINS-PITQRYRLRFRYASSRDARVILVTGAAGTGVGGQVSVN 551
Qy 588 DELVIYINKTKNDDLLTYOTFDLATTNSMGFS-----GDKNELIIGAESFVSNEKIY 641
Db 552 ----MPLQKTMEIGENLTSTFRYTFDSNPFSPRANPDIIIGISEQPLFGAGS-ISSGELY 606
Qy 642 IDKIEFI 648
Db 607 IDKIEII 613
RESULT 17
S02134
parasporal crystal protein cryIC1 - Bacillus thuringiensis (strain aizawai IC1)
N:Alternate names: delta-endotoxin IC1; entomocidal crystal protein
C:Species: Bacillus thuringiensis
A:Variety: strain aizawai IC1
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S02134; S04994
R:Haider, M.Z.; Ellar, D.J.
Nucleic Acids Res. 16, 10927, 1988
A:Title: Nucleotide sequence of a Bacillus thuringiensis aizawai IC1 entomocidal crystal protein
A:Reference number: S02134; MUID:89083518; PMID:3205732
A:Accession: S02134
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-1155 <H>
A:Cross-references: UNIPROT:P06578; EMBL:X13233; NID:g40277; PIDN:CAA31620.1; PID:g40278
A:Experimental source: strain aizawai IC1
R:Haider, M.Z.; Ellar, D.J.
J. Mol. Biol. 208, 183-194, 1989
A:Title: Functional mapping of an entomocidal delta-endotoxin. Single amino acid changes in the C-terminal region of the delta-endotoxin of Bacillus thuringiensis strain aizawai IC1
A:Reference number: S04994; MUID:89362455; PMID:2769751
A:Accession: S04994
A:Molecule type: DNA
A:Residues: 429-449, 'A', 451-724 <HAW>
A:Cross-references: EMBL:X16315
A:Experimental source: strain aizawai IC1
C:Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin
Query Match 26.6%; Score 906.5; DB 2; Length 1155;
Best Local Similarity 33.5%; Pred. No. 6.7e-50;
Matches 221; Conservative 120; Mismatches 228; Indels 91; Gaps 24;
Qy 31 DNPNSTLEELNYKEFLRMTESSSTEVLDNSTVKDVGTVGISVVG-----QILGVGVGVP 84
Db 3 NNPIN-ECIPY-----NCLSNPEVEVLGGERIE-----TGYTIDISLSITQFLSEFVPG 53
Qy 85 AGALTSFYQSFLNTIWN-----PSDADPDKAFMAQVEVLIDKKIEYAKSKALAEQLQNN 140
Db 54 AG-----FVLGLVDIIGIFGPSQ---WDAFLVQIEQLINQRIEFAFNQAISRLGLESLN 106
Qy 141 FEDYVYALNSWKKTPLSLRSKRSQDRIRLFSQAESHFRNSMPSFAVSKFVLFLPTVAQ 200
Db 107 YQIVAESFWEADPTN-PALREMRIQ--FNDMNSALTUATPLFAVQNYQVPLLSVVYQ 163
Qy 201 AANTHLLLLKDAQVFGREWGYSSEDAEFYHRLKLTQQYTDHCVNWNVYVGLNGRSTY 260
Db 164 AANLHLSURDVSFQGRWGFDAATINSRYNDLTRIGNYTDHAVRWYNTGLERWGPDS 223
Qy 261 DAWKFNRRREMTLVLDLVLVFPFYDIRLYSKGVKTELTDRIDTDFSLNTLQEYGP 320
Db 224 RDWIRYNQRRRELTVLVDIVSLFNFYDSRTYPIRTVSQLTREIYTNPV-----LENFG 278

C:Genetics:

A:Gene: cry-1-2; bt2
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin
F:82-586/Product: toxic peptide #status predicted <TXP>
F:82-300/Region: toxic #status predicted
F:300-586/Region: insecticidal #status predicted

Query Match 26.4%; Score 899.5; DB 2; Length 1155;
Best Local Similarity 33.3%; Pred. No. 1.9e-49;
Matches 220; Conservative 118; Mismatches 231; Indels 91; Gaps 24;

Qy 31 DNPNSLEELNYKEFLRMTESSSTVLDNSTVYKDAVGTGISVVG-----QILGVVGVPP 84
Db 3 NNPIN-ECIPY-----NCLSNPEVEVLGGERIE---TGYPIDISLSLTQFLSEFVPG 53
Qy 85 AGALTFFYOSFLNTIW-----PSDADPWKAFMAQVEVLIDKKEEYAKSKALAEQLQNN 140
Db 54 AG-----FVLGLVDIILWIGIFGFSQ---WDAFLVQIEQLINQRIEFAFARNOAISRLGLSNL 106
Qy 141 FEDYVNALNWKKTPLSLRSKRSQDRIRELFSQAESHFNSMPSFAVSKFEVFLFPTYQA 200
Db 107 YQIYAESFREWEADPTN--PALREEMRIQ---FNDMNSALTTAIPLEAVONYQVPLLSTVYVQ 163
Qy 201 AANTHLLLLKDAQVFGEEWYGSSEDAEYFHRQLKLTQOYTDHCYNNVYVGLNGLRGSTY 260
Db 164 AANLHLSVLDRVSVFGQWGFDAATINSRYNDLTRIGNYTDHAVRWYNTGLERVWGPDS 223
Qy 261 DAWVKENRRREMTLTVDLIVLPFYDRLYKGVKTELTRDIFTDPIFSLNTLQEQYCP 320
Db 224 RDMIRYNQFRRELTLVDIVSLFPNYDSRTPIRVTSQUTREIYTNPV-----LENFDG 278
Qy 321 TP-----LSIENSIRKPHLDYLGQIEBHTRLOQYFGKDSFNWMSGNYVETSPSGSKT 376
Db 279 SFRGSAQIEGSIKSPHMLDILNSITITDAHRGEY-----YWSGHQIMASPVGFSPE 332
Qy 377 ITSPPFYGDK-STEPVQKLSFD-COKYVRTIANTDVAAMPNGKVY-----LGVTKVDFSQY 429
Db 333 FTFFPLYGTMGNAAPQORIVAQLGQGVYRTLSST-----LYRRPFNIGINNQLSVL 383
Qy 430 DDQKNETSTOT-----YDSKRNGHVSAQDSIDQLPETTDEPLEKAYSHQINYAECFL 483
Db 384 DGTFFAYGTSNLPASVY---RKSQTV---DSLDEIPQNNVPPRQGFSHRLSHVSMFR 437
Qy 484 MQDRRGTI-----PFFTWTHRSVDFNTIDAETITQLPVVKAYALSSGASIIIEGPGFTG 538
Db 438 SGFSNSSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQPLTKSTNLGSGTSVVKGPFTG 497
Qy 539 NLLFLKSSNSIAKFKVTLSAALLQRYRVRIRYASTTNLRLFVQ-----NSNNDFLVI 592
Db 498 DIL-RTTSPGQISTLRVNI--TAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGN-----550
Qy 593 YINKTMNKDDDLTYQTFDLATNNSNMGFSGDKNELIIGAESFVNSKEIYIDKIEPIPVQL 652
Db 551 -FSATMSGSNLQSGSFRVTGFTFPFNSGSSVFTLSAHVFNSGNEVYIDRIEFVPAEV 609

RESULT 20

A29125
parasporal crystal protein Bt2 - *Bacillus thuringiensis* subsp. *kurstaki* (strain HD-1)
C:Species: *Bacillus thuringiensis* subsp. *kurstaki*
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C:Accession: A29125
R:Fishchoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederm
Bio/Technology 5, 807-813, 1987
A:Title: Insect tolerant transgenic tomato plants.
A:Reference number: A29125
A:Accession: A29125
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-1156 <FIS>
A:Cross-references: UNIPROT:Q9F296; UNIPROT:Q93721
C:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

Query Match 26.4%; Score 899.5; DB 2; Length 1156;
Best Local Similarity 33.3%; Pred. No. 1.9e-49;
Matches 220; Conservative 118; Mismatches 231; Indels 91; Gaps 24;

Qy 31 DNPNSLEELNYKEFLRMTESSSTVLDNSTVYKDAVGTGISVVG-----QILGVVGVPP 84
Db 3 NNPIN-ECIPY-----NCLSNPEVEVLGGERIE---TGYPIDISLSLTQFLSEFVPG 53
Qy 85 AGALTFFYOSFLNTIW-----PSDADPWKAFMAQVEVLIDKKEEYAKSKALAEQLQNN 140
Db 54 AG-----FVLGLVDIILWIGIFGFSQ---WDAFLVQIEQLINQRIEFAFARNOAISRLGLSNL 106
Qy 141 FEDYVNALNWKKTPLSLRSKRSQDRIRELFSQAESHFNSMPSFAVSKFEVFLFPTYQA 200
Db 107 YQIYAESFREWEADPTN--PALREEMRIQ---FNDMNSALTTAIPLEAVONYQVPLLSTVYVQ 163
Qy 201 AANTHLLLLKDAQVFGEEWYGSSEDAEYFHRQLKLTQOYTDHCYNNVYVGLNGLRGSTY 260
Db 164 AANLHLSVLDRVSVFGQWGFDAATINSRYNDLTRIGNYTDHAVRWYNTGLERVWGPDS 223
Qy 261 DAWVKENRRREMTLTVDLIVLPFYDRLYKGVKTELTRDIFTDPIFSLNTLQEQYCP 320
Db 224 RDMIRYNQFRRELTLVDIVSLFPNYDSRTPIRVTSQUTREIYTNPV-----LENFDG 278
Qy 321 TP-----LSIENSIRKPHLDYLGQIEBHTRLOQYFGKDSFNWMSGNYVETSPSGSKT 376
Db 279 SFRGSAQIEGSIKSPHMLDILNSITITDAHRGEY-----YWSGHQIMASPVGFSPE 332
Qy 377 ITSPPFYGDK-STEPVQKLSFD-COKYVRTIANTDVAAMPNGKVY-----LGVTKVDFSQY 429
Db 333 FTFFPLYGTMGNAAPQORIVAQLGQGVYRTLSST-----LYRRPFNIGINNQLSVL 383
Qy 430 DDQKNETSTOT-----YDSKRNGHVSAQDSIDQLPETTDEPLEKAYSHQINYAECFL 483
Db 384 DGTFFAYGTSNLPASVY---RKSQTV---DSLDEIPQNNVPPRQGFSHRLSHVSMFR 437
Qy 484 MQDRRGTI-----PFFTWTHRSVDFNTIDAETITQLPVVKAYALSSGASIIIEGPGFTG 538
Db 438 SGFSNSSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQPLTKSTNLGSGTSVVKGPFTG 497
Qy 539 NLLFLKSSNSIAKFKVTLSAALLQRYRVRIRYASTTNLRLFVQ-----NSNNDFLVI 592
Db 498 DIL-RTTSPGQISTLRVNI--TAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGN-----550
Qy 593 YINKTMNKDDDLTYQTFDLATNNSNMGFSGDKNELIIGAESFVNSKEIYIDKIEPIPVQL 652
Db 551 -FSATMSGSNLQSGSFRVTGFTFPFNSGSSVFTLSAHVFNSGNEVYIDRIEFVPAEV 609

RESULT 21

A42459
parasporal crystal protein cry1Fa1 - *Bacillus thuringiensis* (strain aizawai)
N:Alternate names: parasporal crystal protein cry1F
C:Species: *Bacillus thuringiensis*
C:Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C:Accession: A42459
R:Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C.
J. Bacteriol. 173, 3966-3976, 1991
A:Title: Isolation and characterization of a novel insecticidal crystal protein gene from
C:Reference number: A42459; MUID:91286178; PMID:2061280
A:Accession: A42459
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1174 <CHA>
A:Cross-references: UNIPROT:Q03746; GB:M63897; NID:g142757; PIDN:AAA22348.1; PID:g142758
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 26.4%; Score 898.5; DB 2; Length 1174;
Best Local Similarity 34.5%; Pred. No. 2.2e-49;
Matches 204; Conservative 104; Mismatches 221; Indels 63; Gaps 14;

QY 82 VPPAGALTSFYQSFLNTIWPSSADPWKAFMAQVEVLIDKKIEEYAKSKALAEQLQNNF 141
DB 49 VPGVGAFGLFDLWGLITSD---NSLFLQLIQLEQRIETLERNRAITTLRLGLADSY 105
QY 142 EDYVNALNSWKKTPLSLRSKRSQDRIRBELFSQAESHFRNSMPSFAVSKFVFLPPTYQA 201
DB 106 EIVIEALLREWEANP---NNAQLREDVRIREFANTDDALITAINNFTLTSFPIPLSVVQA 162
QY 202 ANTHLLLLKDAQVGEWGYSSSEDVAEFYHRLKLTQOYTDHCVNWNVNGINGLRGSTDYD 261
DB 163 ANLHLSLLRDAVFGQGWGLDIAIATNNHYNRLNLHRYTKGLCDTYNQGLENLRGNTNR 222
QY 262 AWKFNFRFRREMITLVLIDLVPFPFYDIRLYSKGVKTELTRDIFDPIFSLNTLOEYGP 321
DB 223 QWAFNQFRDLTLVLIDVALFPNYDVRYPIQTSQLTREIYTSVIEDSPVANIPN 282
QY 322 -FUSIENSIRKPHLFDYLOQIEBHT----RLQPGYFGKDSFNWYSGVNYVETRPSIGSSKT 376
DB 283 GFNRAEFGVPPHLMDFMNSL-FVTAETVRSQ-----TWGGLVSSRNAGN--R 330
QY 377 ITSPFVY-----DKSTPQVQLSFDGQKVYRTIANTDV--AAWNGKVYLGVTX 423
DB 331 INFPSYGVFNPGGAIWADEDRP-----FYRLSDPVFVRGCGFNPHYVLGLRG 380
QY 424 VDFSDYDQKNETSTQFYDSKRNNGHVSAQDSIDQLPPETTDDEPLEKAYSHQNLNABCF- 482
DB 381 VAQQ-----TGNHRTFRNSGTI---DSLDEIPQNSGAPWMDYSHVLNHTFVR 430
QY 483 -----LMODRRGTIPFPFWTHRSVDFFNTIDAETITQLPVVKAVALSGSASIIEGPGFTGG 538
DB 431 WPGEISGDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGG 490
QY 539 NLLFLKSSNSIAKFKVTLNSALLQRYRIRYASTNLRFLVQNSNNDPLVIYINKTM 598
DB 491 DI--LARTSGGPAYTIVNGQLPQRYRIRYASTNLRIRYTVVAGERIFAPQGFNKT 548
QY 599 NKDDDLTYQTFDLATNNSMGFGSKNELIIGAESFVSNKIEYIDKIEPIPV 650
DB 549 DTGDLPTFQSFVSATINTATTFMWSQSSFTVGADTFSSGNEVIDRPELIPV 600
RESULT 22
I39838
paraasporal crystal protein - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: I39838
J;Hefford, M.A.; Brousseau, R.; Prefontaine, G.; Hanna, Z.; Condie, J.A.; Lau, P.C.K.
A;Title: Sequence of a lepidopteran toxin gene of Bacillus thuringiensis subsp kurstaki
A;Reference number: I39838
A;Accession: I39838
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1155 <RES>
A;Cross-references: UNIPROT:P06578; GB:M37263; NID:g142885; PIDN:AAA22420.1; PID:g142886
C;Superfamily: paraasporal crystal protein
C;Keywords: delta-endotoxin
Query Match 26.3%; Score 895.5; DB 2; Length 1155;
Best Local Similarity 33.3%; Pred. No. 3.4e-49;
Matches 220; Conservative 118; Mismatches 231; Indels 91; Gaps 24;
QY 31 DNPNSTLEENLYKEFLRMTSDSTEVLDNSTVDKAVGTGTSVVG-----QILGWGVGVPF 84
DB 3 NNPNIN-ECIPY-----NCLSNPEVILGGERIE---TGYPIDISLSLQFLISEFVPG 53
QY 85 AGALTSFYQSFLNTIWPSSADPWKAFMAQVEVLIDKKIEEYAKSKALAEQLQNN 140
DB 54 AG-----FVLGLVDIIMGIFPSQ---WDAFLVQIEQLINQRIEFAFNQAIISRLGSLN 106
QY 141 FEDYVNALNSWKKTPLSLRSKRSQDRIRBELFSQAESHFRNSMPSFAVSKFVFLPPTYQA 200

DB 107 YQIVAESFREWEADPTN-PALREEMRIQ--ENDMNSALTTTAPLFAVQNVQVPLSVVQ 163
QY 201 AANTHLLLLKDAQVGEWGYSSSEDVAEFYHRLKLTQOYTDHCVNWNVNGINGLRGSTDY 260
DB 164 AANLHLSLVLRDVSFVGQWGFDAATINSRYNDLTRLIGNYTDHAVRYNTGLERWGPDS 223
QY 261 DAMVKFNFRFRREMITLVLIDLVPFPFYDIRLYSKGVKTELTRDIFDPIFSLNTLOEYGP 320
DB 224 RDMIRYNOFRRELTTLVLIDVALFPNYDVRYPIQTSQLTREIYTNPV-----LENPDG 278
QY 321 TF-----LSIENSIRKPHLFDYLOQIEBHTRLQPGYFGKDSFNWYSGVNYVETRPSIGSSKT 376
DB 279 SPRGSAQIEGSIKSPHMLDILNSITITTDARHEY-----YWSGHQIMASPVGFSQPE 332
QY 377 ITSPFVYCDK-STEPVQKLSFD-CQKVYRTIANTDVAAWNGKVY-----LGVTKVDFSOY 429
DB 333 FTFPLTYGTMGNAAPQQRIVQAQGGVYRTLSST-----LYRRPFTGINNQQLSVL 383
QY 430 DDOKNETSTOT-----YDSKRNNGHVSAQDSIDQLPPETTDDEPLEKAYSHQNLNABCF 483
DB 384 DGTPEYAGTSSNLPASVY---RKSGTV---DSLDEIPQNNVUPPROGFRHRLSHVSMFR 437
QY 484 MODRRGTI-----PFTFWTHRSVDFFNTIDAETITQLPVVKAVALSGSASIIEGPGFTGG 538
DB 438 SGFSNSSVSIIRAPMFSWIHRSANFNIIIPSSQITQIPLTKSTNLGSGTSVVRGPGFTGG 497
QY 539 NLLFLKSSNSIAKFKVTLNSALLQRYRIRYASTNLRFLVQ-----NSNNDPLVI 592
DB 498 DIL-RRTPSQISTLVRNI-TAPLSQRYRIRYASTNLRFLVQ-----HGRPINQGN----- 550
QY 593 YINKTNKKDDDLTYQTFDLATNNSMGFGSKNELIIGAESFVSNKIEYIDKIEPIPVOL 652
DB 551 -PSATWSSGNSLQSGFRHLGFTTTPNFNSGSSVFTLSAHVFNSGNEVYIDRIEFVPAEV 609
RESULT 23
A41052
paraasporal crystal protein cryAel - Bacillus thuringiensis (strain alesti)
C;Species: Bacillus thuringiensis
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
C;Accession: A41052
R;Lee, C.S.; Aronson, A.I.
J;Bacteriol. 173, 6635-6638, 1991
A;Title: Cloning and analysis of delta-endotoxin genes from Bacillus thuringiensis subsp
A;Reference number: A41052; MUID:92011442; PMID:1655719
A;Accession: A41052
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1181 <LEES>
A;Cross-references: UNIPROT:Q03748; GB:M65252; NID:g142874; PIDN:AAA22410.1; PID:g142875
C;Superfamily: paraasporal crystal protein
C;Keywords: delta-endotoxin
Query Match 26.1%; Score 888; DB 2; Length 1181;
Best Local Similarity 34.6%; Pred. No. 1.1e-48;
Matches 206; Conservative 107; Mismatches 222; Indels 60; Gaps 18;
QY 82 VPPAGALTSFYQSFLNTIWPSSADPWKAFMAQVEVLIDKKIEEYAKSKALAEQLQ 137
DB 51 VPGAG-----FVLGLIDLINGFVGPSQ---WDAFLVQIEQLISQRIEFAFNQAIISRL 103
QY 138 QNNFEDYVNALNSWKKTPLSLRSKRSQDRIRBELFSQAESHFRNSMPSFAVSKFVFLPT 197
DB 104 SNLYQIYAEAFREWEADPTN-PALREEMRIQ--FNDMNSALTTTAPLFTVQNVQVPLSV 160
QY 198 YQAQANTHLLLLKDAQVGEWGYSSSEDVAEFYHRLKLTQOYTDHCVNWNVNGINGLRG 257
DB 161 YQAVNLHLSVLRDVSFVGQWGLDVATINSRYNDLTRLIGTYTDYAVRYNTGLERVWG 220
QY 258 STYDAWVKFNFRREMITLVLIDLVPFPFYDIRLYSKGVKTELTRDIFDPIFSLNTLOE 317
DB 221 PDSRDWRYNQFRRELTTLVLIDVALFPNYDVRYPIQTSQLTREIYTNPV-----LEN 275

| | | | |
|--|-----|---|-----|
| QY | 318 | YGPTFLS-----IENSIRKPHFLDYLVQGLIEFTRLOQYFGKDSFNYSWGNVETRPSIGS | 373 |
| Db | 276 | PDGSRGSAQRIEQIRSPHMLDILNSITYTDAGGYY-----YWSGHIWASPVGFS | 329 |
| QY | 374 | SKTITSPFYGDK-STPEVQKLSFD-GQVYRTIANTDVAAMPNGKAVLYGVTKVDFSQYDD | 431 |
| Db | 330 | GPEFTPLVGTWGNAAPOQRIVAQLCGQYRTLSST-----FYRNPFIIGNQRLSLVDG | 385 |
| QY | 432 | QK---NETSTQTYDSKRNGHVSQAODSIDQLPPETTDPELEKAYSHQINVAECFLMQDRR | 488 |
| Db | 386 | TEFAYGSSNLPSAVYRKSQTV---DSLDEIPQDNNVPPRQGFSHRLSHVSMRFSFSN | 442 |
| QY | 489 | GTI-----PFFTWTHTSRVDFFNTIDAEXTLPVVKAKALSSGASIIIEGPGFTGNNLFL | 543 |
| Db | 443 | SSVSIIRAPMFSWIHRSABFNIIIPSSQITPLTKSNLGSSTSVVKSGPGFTGDDIL-R | 501 |
| QY | 544 | KSSNSIAKFKVTLNSAALLQRYRIRYASTTNLRLFVQ-----NSNDFLVIYINKT | 597 |
| Db | 502 | RTPSQISTLRVNI-TAPLSQRYRIRYASTTNLQFHTSIDGRPINQGN-----FSAT | 554 |
| QY | 598 | MNKDDDLTYQTFLATTNMGFSGDKNELIIGABSEFVSNKEIYIDKIEFIPVOL | 652 |
| Db | 555 | MSSGGLQSGSFRVTGFTTFFNFSGSSVFTLSAHVFNSEGNVEYIDRIEFVPAEV | 609 |
| RESULT 24 | | | |
| A48970 | | | |
| parasporal crystal protein cryIcB - Bacillus thuringiensis | | | |
| C:Species: Bacillus thuringiensis | | | |
| C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004 | | | |
| C:Accession: A48970 | | | |
| R:Kaltman, S.; Kiehn, K.L.; Libs, J.L.; Yamamoto, T. | | | |
| Appl. Environ. Microbiol. 59, 1131-1137, 1993 | | | |
| A:Title: Cloning of a novel cryIC-type gene from a strain of Bacillus thuringiensis subsp. | | | |
| A:Reference number: A48970; MUID:93236401; PMID:8476286 | | | |
| A:Accession: A48970 | | | |
| A:Status: preliminary | | | |
| A:Molecule type: nucleic acid | | | |
| A:Residues: 1-1176 <KAL> | | | |
| A:Cross-references: UNIPROT:P56953; GB:M97880; NID:g289263 | | | |
| A:Experimental source: subsp. galliariae HD29 | | | |
| A:Note: sequence extracted from NCBI backbone (NCBIN:129672, NCBIP:129675) | | | |
| C:Superfamily: parasporal crystal protein | | | |
| C:Keywords: delta-endotoxin | | | |
| Query Match 26.0%; Score 886.5; DB 2; Length 1176; | | | |
| Best Local Similarity 36.7%; Pred. No. 1.3e-48; | | | |
| Matches 226; Conservative 103; Mismatches 220; Indels 67; Gaps 24; | | | |
| QY | 60 | STVKDAVGTGISVVGQILGVGVPPAGALTSFYQSFLNTIWPSPADPWKAFMAQVEVLID | 119 |
| Db | 29 | STGNSSIDISLSIV-QLLVSNFVPGG3FLVGLLDFVWGIVGFS---PMDAFLVQIEQLIN | 84 |
| QY | 120 | KTIEEYAKSKALAEQGLONNPFEDVYNALNSWKTKPLSLRSKRSQDRIRLEFSAQSHFR | 179 |
| Db | 85 | ERIAAYARSAATLSNLEGLGNNFIYVEAFKEWADP---DNPVTRVVDVDFRILDCGLE | 141 |
| QY | 180 | NSMPSFVSKFVFLPTVYQAANTHLLLLKDAQVGEWGSYSDVAEFYHRLQKLTQ | 239 |
| Db | 142 | RDIPSPRIAGFEVPLLSVYQAANLHLAILRDSISIFGARWGLTITINNENYRILRHIDE | 201 |
| QY | 240 | YTDHCNVTNVLNGLRGSTYDAWKFNRFREMTLTVLDLVLPPFYDILYSGVKVTE | 299 |
| Db | 202 | YANHCAADTYNRGLNLPKSTYQDMYTNKRLRDLTLVLDIAAFPSYDNRNRYPIQSVGQ | 261 |
| QY | 300 | LTRDIFDTPISLN-TLOEYQ--PTFLSIE-NSIRKPHFLDYLVQGLIEFTRLOQYFGKD | 355 |
| Db | 262 | LTRIEYTDPLITNPQLQSVQALPTFNVMESNAIRTPHLFDVNLNLTFT-----DMFSVG | 317 |
| QY | 356 | SPNYSWGNVETRPSIGSKTITSPFYG-DKSTPEVQKLSFDGOKVYRTIANTDV-----A | 410 |
| Db | 318 | RNFYWGCHRVISN-RIGGG-NITSPYIGREANQEPFRPTFNG-PVFRTLSNPTFRPLQ | 374 |
| QY | 411 | AVPNKGVYL-GVTKVDFSQYDDQKNETSTQTYDSKRNGHVSQAODSIDQLPPETTDPELE | 469 |
| Db | 375 | PWPAPFPNLRGVEGFEFS-----TPLNSFTY---RGRGTV---DSLTELPPEDNSVPPR | 422 |
| QY | 470 | KAYSHQINVAECFLMQDRGTI-----PFFTWTHTSRVDFFNTIDAEXTLPVVKAYALS | 524 |
| Db | 423 | EGYSHRLCHA---TFVQRSGTPLFTGPFVFSWTHRSATDRNLIYPDVINQIPLVKAFNLT | 479 |
| QY | 525 | SGASIEGPGFTGNNLFLKSSNSIAKFKVTLN-SAALLQRYRIRYASTTNLRLFV- | 582 |
| Db | 480 | SGTSVVRGPGFTGDIIRTNVNGSVLS---MSLNFSNTTQRYRIRYASTTNVMSVT | 536 |
| QY | 583 | -----QNSNDFLVIYINKTMKDDDLTYQTFLATTNMGFSGDKNELIIGABSEFVSN- | 637 |
| Db | 537 | VGSSTTGNQGF-----PSTMSANGALTQSFRFAEPFVGVISASGSQ-----GASISISNN | 586 |
| QY | 638 | ---EKIYIDKIEFIPV | 650 |
| Db | 587 | VGRQMFHLDRIEFLPV | 602 |
| RESULT 25 | | | |
| JT0241 | | | |
| parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7) | | | |
| N:Alternate names: 135K insecticidal protein | | | |
| C:Species: Bacillus thuringiensis | | | |
| C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004 | | | |
| C:Accession: JT0241 | | | |
| R:Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H. | | | |
| Agric. Biol. Chem. 52, 1565-1573, 1988 | | | |
| A:Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein | | | |
| A:Reference number: JT0241 | | | |
| A:Molecule type: DNA | | | |
| A:Residues: 1-1176 <SHI> | | | |
| A:Cross-references: UNIPROT:P02965 | | | |
| A:Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal protein | | | |
| C:Comment: The 135K protein has insecticidal activity against Plutella xylostella larvae | | | |
| C:Superfamily: parasporal crystal protein | | | |
| C:Keywords: delta-endotoxin | | | |
| Query Match 25.7%; Score 876; DB 2; Length 1176; | | | |
| Best Local Similarity 32.9%; Pred. No. 6.2e-48; | | | |
| Matches 215; Conservative 120; Mismatches 240; Indels 78; Gaps 22; | | | |
| QY | 31 | DNPNSTLEELNYKBFIRMTEDSSTEVLDSNVTKDAVGTGISVVG-----QILGVGVGVPF | 84 |
| Db | 3 | NNPNIN-ECIPY---NCLSNPEVEVLGGERIE---TGYTPIDISLSLTQFLSEFVPG | 53 |
| QY | 85 | AGALTSFYQSFLNTIWN-----PSDADPWKAFMAQVEVLIDKIEEYAKSKALAEQGLQNN | 140 |
| Db | 54 | AG---FVLGLVDIIGIFGFSQ---WDALFVQIEQLINQRIEFARNOAISRLGLESLN | 106 |
| QY | 141 | FEDYVNALNSWKTKPLSLRSKRSQDRIRLEFSAQSHFRNSMPSFAVKFVFLPTVYQ | 200 |
| Db | 107 | YQIYAESFREWEADPTN-PALREEMRIQ--FNDMNSALTTAIPLFAVQYVPLLSVTVQ | 163 |
| QY | 201 | AANTHLLLLKDAQVGEWGSYSDVAEFYHRLQKLTQYTDHCNVTNVLNGLRGSTY | 260 |
| Db | 164 | AANLHLSVLDRVSVFGQWGFDAATINSRYNDLTLRLIGNYTDYAVRWNTGLERWVGSDS | 223 |
| QY | 261 | DAWKFNRFREMTLTVLDLVLFPFYDILYSGVKTELTDRDIFDTPISLNTIOEYGP | 320 |
| Db | 224 | RDWRYNQFRETULTVLIDIVALFSYDSERYPIRTVSQLTREIVTNPV-----LENFDG | 278 |
| QY | 321 | TFLS-----IENSIRKPHFLDYLVQGLIEFTRLOQYFGKDSFNYSWGNVETRPSIGSKT | 376 |
| Db | 279 | SFRGMAQRIBQNIQRPHLMDILNSITITVDVHRG-----FNWSGHQITASPVGSGPE | 332 |
| QY | 377 | ITSPFYGDK-STPEVQKLSFDGOKVYRTIAN-----TDVAAMPNGKVYLGVTKVDFSQYD | 430 |
| Db | 333 | FAPFLFCNAGNAAPPVVLVSLTGLIGIFETLSSPLRYRILILGSGNNQELFVLDCGTESFPAS | 392 |

Db 503 SPGQISTLRVNI-TAPLSQRYRVRIRYASTINLQFHTSIDGRPINQGN-----FSATWS 555
 Qy 600 KDDDLTYQTFDLATNNSMGFSQDKNELIIGAESFVSGNEKIYIDKIEFIPVOL 652
 Db 556 SGNLQSGSPTVGFTTFPNSGSSVFTLSAHVFNSGNEVYIDRIEFVPAEV 608

RESULT 28
 I40572
 parasporal crystal protein cryICb - Bacillus thuringiensis
 C:Species: Bacillus thuringiensis
 C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
 C:Accession: I40572
 R:Boesse, M.; Masson, L.; Brousseau, R.
 Nucleic Acids Res. 18, 7443, 1990
 A:Title: Nucleotide sequence of a novel crystal protein gene isolated from Bacillus thuringiensis
 A:Reference number: I40572; MUID:91081338, PMID:2259636
 A:Accession: I40572
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1171 <RES>
 A:Cross-references: UNIPROT:Q57458; EMBL:X56144; NID:G40281; PIDN:CAA39609.1; PID:G40282282
 C:Genetics:
 A:Gene: cryIC(b)
 C:Superfamily: parasporal crystal protein
 C:Keywords: delta-endotoxin

| | Query Match | 25.5% | Score 869.5; | DB 2; | Length 1171; |
|----|-----------------------|-------------------|----------------------------|---------------------|----------------------------|
| | Best Local Similarity | 33.7% | Pred. No. 1.6e-47; | | |
| | Matches 219; | Conservative 117; | Mismatches 241; | Indels 73; | Gaps 21; |
| Qy | 19 | ELQTNHQ--- | YPLADNPNSLTLELNKYEFRTMTEDS | TEVLDNSTVKDAVG | GTGISVVGQ 75 |
| Db | 2 | EIVANNQCV | PNCLNPN----- | EILDERSNSTVAT | NIALEIS 42 |
| Qy | 76 | ILGVGVFP | PAGALTSFYOSFLNTIWP | SADDPKAFMAQVEVLIDK | IEEYAKSALAEQ 135 |
| Db | 43 | RLLASATPI | GIGLILGLFDPAIWGSIGPSQ--- | WDLFLEQIELLIDQKIEE | FARNQAISRLE 99 |
| Qy | 136 | GLQNNFEDY | VNALMSWKTPLSLRSKSQDRI | RELFSQAESHFNPSFV | AFVFL 195 |
| Db | 100 | GISLSYGI | YTEAFREWEADPTNPALK--- | EEMRTOFQDNMSILVTALP | FLSFVQNYQVPEL 156 |
| Qy | 196 | PTYQAANTH | LLLLKDAOVFEEGWCYSS | EDVAEPVHRQLKTOQYD | HCVVNWNVLN-- 253 |
| Db | 157 | SVYVOAAM | LHLVSLVDVSVFGANGFD | TIATNSRNDLTRLIPIY | TDVAVRWYNTGLDRL 216 |
| Qy | 254 | ---GLRGSTY | DAAWKFNRFREMTLTVDL | IVLPFFYDILKSGVKV | TELTROIPTDPI 309 |
| Db | 217 | PRTGGLRN---- | WARFNQFRRELTISVLDI | ISIISFRNYDSRLYPI | PTSSQLTREYTPDV 271 |
| Qy | 310 | PSLNTLQ | EYGPTELSIENS-IRKPHL | FYDYLQIEPHTRLQCY | FGKDSFNWWSGNYVETR 368 |
| Db | 272 | INI-TDYRV | GSFSENIENSIRSPHMLD | FLNNLTITD | DLIRG-----VHWAGHRV-TS 323 |
| Qy | 369 | PSIGSKTIT | PFYFG-DKSTPE---VQLS | FDGQKV-YRTIANTDVA | AMPNGKVLGVTK 423 |
| Db | 324 | HFTGSSQV | ITTPQYGITANAEPRTI | APSTPGLNLFVRTLSN | PPFRSENITPTLGIV 383 |
| Qy | 424 | VDFSQYDQ | KNETSTQTVDSKENNGH | VSAQSDIDOLPPE | TTEPLEKAYSHOLNVAEC-- 481 |
| Db | 384 | VQGVGFI | QPNN--AEVLY---RSRGT | V---DSLNELPIDGEN | SLV--GYSHRLSHVTLTR 433 |
| Qy | 482 | FLMQDRRG | TIPFTWTHRSVDPFNT | IDAETITQLPFWKAY | ALSSGASITIEGPTGGNLL 541 |
| Db | 434 | SLYNTNIT | SLPTFVWTHSATNTNIN | PDIIITQIPLVKG | FRLGGGTSVIKGPPTGGDIL 493 |
| Qy | 542 | FLKESNS | IAKF---KVTLSAALLQ | RYRVRIRYASTNLR | LFVQNSNDFLVIYINKTM 598 |
| Db | 494 | ----RNTT | IGEVSQVNIINS-PITQ | RYLRFRFYASSR | DARITVAIGGOIRVDMTLEKTM 548 |
| Qy | 599 | NKDDTLT | YOTFDLATNNSMGFSQ | KNELIIGAESFVSG | NEKIYIDKIEFI 648 |

Db 549 EIGESLTSRTFSYTNFNSPFRANPDIIIRAEELPIRGELYIDKIELI 598

RESULT 29

A37829

parasporal crystal protein cry1Ba1 - Bacillus thuringiensis

C;Species: Bacillus thuringiensis

C;Date: 14-Jun-1991 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

C;Accession: A37829; S13762; S14438

R;Visser, B.; Munsterman, E.; Stoker, A.; Dirkse, W.G.

J. Bacteriol. 172, 6783-6788, 1990

A;Title: A novel Bacillus thuringiensis gene encoding a Spodoptera exigua-specific crystal protein

A;Reference number: A37829; MUID:91072224; PMID:2254254

A;Accession: A37829

A;Molecule type: DNA

A;Residues: 1-1171 <VI2>

A;Cross-references: UNIPROT:O06894; EMBL:X53985

A;Note: translation is incomplete

C;Superfamily: parasporal crystal protein

C;Keywords: delta-endotoxin

Query Match 25.5%; Score 869.5; DB 2; Length 1171;

Best Local Similarity 33.7%; Pred. No. 1.6e-47;

Matches 219; Conservative 117; Mismatches 241; Indels 73; Gaps 21;

Qy 19 ELQTHNQ--YPLADNPSTLEELNYKEFLRMTESSTEVLNDSTVKDAVGTGISVVGQ 75

Db 2 EIVNNQOCVPCNLPNEN-----EILDIERSNSTVATNIALEIS 42

Qy 76 ILGVGVFPFAGALTSFYOSFLNTIWPSPADPWKFAQVEVLIDKIEEYAKSALAEQ 135

Db 43 RLLASATPIGGILLGLFDALWISGIFSQ--WDLFEQIEELLIDQKIEEFARNQAISRLE 99

Qy 136 GLQNNFEDYVNALNSWKKTPLSLRKSRSDRLRELFSQAESHFRSNMPSFAVKFEVLFL 195

Db 100 GISLGYHYTEAFREWEADPTNPAK--EEWRTQPDNMSILVTAIPLESVQNYQVFL 156

Qy 196 PTYQAANTHLLLLKDAQVGEWGYSSDDVAEFYHRQLKLTQOYTDHCNVNWNVLN-- 253

Db 157 SVVYQAANLHLSVLKRDVSVEGQAWGFDIATINSRYNDLTRLIPIYTDYAVRWYNTGLDRL 216

Qy 254 ---GLRGSTDWAKFKENFREEMTLTVLDDLVLPPFYDIRLYSKGVKTELTTRDIFTPI 309

Db 217 PRTGGLRN-----WARENQFRELTVISLDIISFFRNYDSRLPIPTSSQITREYVTDPV 271

Qy 310 FSLNTLQBYGPTFLGIENS-IRKPHLDYLOGIEFHTRLQPGYFGKDSFNWGSNYVETR 368

Db 272 INI-TDYRGVSPFENIENSAIRSPHLMFLNLTIDTLIRG-----VHYWAGHRV-TS 323

Qy 369 PSIGSKVITSPYG-DKSTEP---VOKLSFDGQKV-YRTIANTDVAWNGKVLGVTK 423

Db 324 HFTGSQVITTPQYGITANAEPRTIAPSTFPGLNLFYRTLSPNPPFRRSNITPTGLINLV 383

Qy 424 VDFSQYDDQKNETSTQTYDSKKNNGHVSAQDSIDQLPETTDDBPLEKAYSHQLNYAEC-- 481

Db 384 VQGVGFIQPNV--AEVLY---RSGTV--DSLNELPIDGENSLV--GYSHRLSHVLTIR 433

Qy 482 FLMQDRRGITPFTWTHRSVDFNTIDASKITQLPVVKAYALSSGASIIEGPGTGNLL 541

Db 434 SLYNTNITSLPTFVWTHHSATNTNTNPDIITQIPLVKFRLLGGGTSVIRGPGTGGDIL 493

Qy 542 FLKSSNSNAKE---KVTLNSAALLQRYRIRYASTTNLRLFVQNSNNDFLVYINKMT 598

Db 494 ----RENTIGEFVGLQVNTNS-PITQRYRIRFYASSRDARIITVAIGQIRVDMTLEKTM 548

Qy 599 NKDDDLTYQTFDLATNNSNGFSGDKNELIIGAESFVSNKEIYIDKIEPI 648

Db 549 EIGESLTSRTFSYTNFNSPFRANPDIIIRAEELPIRGELYIDKIELI 598

RESULT 30

A49785

parasporal crystal protein cryIA(c) - Bacillus thuringiensis subsp. kenya (strain HD568)

C;Species: Bacillus thuringiensis subsp. kenya
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: A49785
R;Von Tersch, M.A.; Robbins, H.L.; Jany, C.S.; Johnson, T.B.
Appl. Environ. Microbiol. 57, 349-358, 1991
A;Title: Insecticidal toxins from Bacillus thuringiensis subsp. kenya: gene cloning and
A;Reference number: A49785; MUID:91197102; PMID:2014985
A;Accession: A49785
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1177 <VON>
A;Cross-references: UNIPROT:Q45735; GB:M35524; NID:g142739; PIDN:AAA22338.1; PID:g142740
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 25.5%; Score 867.5; DB 2; Length 1177;
Best Local Similarity 33.7%; Pred.No. 2.2e-47;
Matches 220; Conservative 110; Mismatches 242; Indels 81; Gaps 24;

```
QY 31 DNPNSTLEELNYKEFLRMTESSTEVLDSNSTVDAVGTGISVVG-----QILGVVGVVPF 84
   :||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 3 NNPNN-ECIPY----NCLSNPEVEVLGGERIE----TGYTPDISLSLTQFLSEFVPG 53

QY 85 AGALTSYQSFNTIWM-----PSDADPWKAPMAQVEVLIDKKIEYAKSKALAEQLQGN 140
   || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 54 AG----FVLGLVDIIWGIFGPSQ---WDAFLVQIEQLINQRIEFARNOAISRLGLESLN 106

QY 141 FEDYVNALNSKKTPLSLRKSDQRIELFSQAESHFRNSMPSPFAVSKEVFLFLPYAQ 200
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 107 YQIYAESFWEADPTN-PALREEMRIQ---FNDMNSALTATPILPAVQNVQVPLLSVYVQ 163

QY 201 AANTHLLLLKDAQVFGEEGYSSEDAEFYHRLQKLTQOYTDHCVNVNVLNGLRGSTY 260
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 164 AANLHLSVLRDVSFGQWGFDAATINSRYNDLTRIGNYTDVAVRYNTGLERVWGPDS 223

QY 261 DAWVKNRFRREMTLVLDLILVFPFYDIRLYSKGVKTELTRDFTDPIPSLNTLQBYGP 320
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 224 RDMVRYNQFRRELTTLVLDIVLFPNYDSRRYPVRTVSQLTREIYTNPV-----LENFDG 278

QY 321 TF----LSIENSIRKPHLDYLOGIEFHTLRQYFGKDSFNVMGNYVETRSIGSSKT 376
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 279 SFRGSAQGIERSIRSHPLMDILNSITITYDAHRGY-----YWSGHQIMASPVGFSGPE 332

QY 377 ITSPFFYGDK-STEPVQKLSFD-GQKYVRTIANTDVAAMPNGKVVGLVTKVDFSOYDDQKN 434
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 333 FTFLYGTWGNAAPOQRIVAQLQGQVYRTLSST-----FYRPPNIGINNQQLSVLGTEF 388

QY 435 ETSTQT-----YDSKRNNGHVSAQDSIDQLPETTDEPLEKAYSHQLNYAECLMQDRR 488
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 389 AYGTSSNLPASVY---RKSGTV---DSLDEIPPNNNVPPRQGFSHRLSHVSMF---RS 438

QY 489 GT-----IPFTWTHRSVDFPNTIDAETITQLPVKAYALSSGASIIIEGPGFTGGNL 540
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 439 GSSESVIIRAPMFSWIHRSAEFNNIADSITQIPAVKGNFLFNG-SVISGFGFTGGDL 497

QY 541 LFLKESNSIAK---FKVTLNSAALLQRYVRIRYASTTNLRFVQNSNDFLVIYINKT 597
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 498 VRLNSSGNIIQNGYIEVPFIHFPTSTRYVRVRYASVTPHILNVNMGNSSIFSNVTVPAT 557

QY 598 MNKDDDLTYQTFDLATNNGMFGSKNELIIGAESFVSNEKIYIDKIEFIPV 650
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 558 ATSLDNL--QSSDFGYFESANAFSTSSLGN-IVGVRNFSGTAGVIIDRFEPFIPV 607
```

RESULT 31

USSSXH

parasporal crystal protein cryIaC1 [validated] - Bacillus thuringiensis subsp. kurstaki
C;Species: Bacillus thuringiensis subsp. kurstaki
C;Date: 18-Apr-1984 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A23962; A03489
R;Adang, M.J.; Scaver, M.J.; Rocheleau, T.A.; Leighton, J.; Barker, R.F.; Thompson, D.V.
Gene 36, 289-300, 1985
A;Title: Characterized full-length and truncated plasmid clones of the crystal protein d

A;Reference number: A91526; MUID:86083171; PMID:3000881

A;Accession: A23962

A;Molecule type: DNA

A;Residues: 1-1178 <ADA>

A;Cross-references: UNIPROT:P05068; GB:M11068; NID:g142721; PIDN:AAA22331.1; PID:g142722
A;Experimental source: strain HD-73

A;Note: the authors translated the codon ATT for residue 11 as Leu

R;Wong, H.C.; Schnepf, H.E.; Whiteley, H.R.

J. Biol. Chem. 258, 1960-1967, 1983

A;Title: Transcriptional and translational start sites for the Bacillus thuringiensis cr

A;Reference number: A92410; MUID:83109004; PMID:6296116

A;Accession: A03489

A;Molecule type: DNA

A;Residues: 1-76, 'P', 78-147, 'L', 149-247, 'S', 249-282, 'M', 284-285, 'R', 287-288, 'QN', 291-292

A;Experimental source: strain HD-1

C;Comment: This protein is present in crystalline form as a component of the spore coat.

C;Superfamily: parasporal crystal protein

C;Keywords: delta-endotoxin

Query Match 25.5%; Score 867; DB 1; Length 1178;

Best Local Similarity 33.4%; Pred.No. 2.3e-47;

Matches 219; Conservative 112; Mismatches 240; Indels 84; Gaps 24;

```
QY 31 DNPNSTLEELNYKEFLRMTESSTEVLDSNSTVDAVGTGISVVG-----QILGVVGVVPF 84
   :||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 3 NNPNN-ECIPY----NCLSNPEVEVLGGERIE----TGYTPDISLSLTQFLSEFVPG 53

QY 85 AGALTSYQSFNTIWM-----PSDADPWKAPMAQVEVLIDKKIEYAKSKALAEQLQGN 140
   || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 54 AG----FVLGLVDIIWGIFGPSQ---WDAFLVQIEQLINQRIEFARNOAISRLGLESLN 106

QY 141 FEDYVNALNSKKTPLSLRKSDQRIELFSQAESHFRNSMPSPFAVSKEVFLFLPYAQ 200
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 107 YQIYAESFWEADPTN-PALREEMRIQ---FNDMNSALTATPILPAVQNVQVPLLSVYVQ 163

QY 201 AANTHLLLLKDAQVFGEEGYSSEDAEFYHRLQKLTQOYTDHCVNVNVLNGLRGSTY 260
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 164 AANLHLSVLRDVSFGQWGFDAATINSRYNDLTRIGNYTDVAVRYNTGLERVWGPDS 223

QY 261 DAWVKNRFRREMTLVLDLILVFPFYDIRLYSKGVKTELTRDFTDPIPSLNTLQBYGP 320
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 224 RDMVRYNQFRRELTTLVLDIVLFPNYDSRRYPVRTVSQLTREIYTNPV-----LENFDG 278

QY 321 TF----LSIENSIRKPHLDYLOGIEFHTLRQYFGKDSFNVMGNYVETRSIGSSKT 376
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 279 SFRGSAQGIERSIRSHPLMDILNSITITYDAHRGY-----YWSGHQIMASPVGFSGPE 332

QY 377 ITSPFFYGDK-STEPVQKLSFD-GQKYVRTIANTDVAAMPNGKVV-----LGVTKVDFSOY 429
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 333 FTFLYGTWGNAAPOQRIVAQLQGQVYRTLSST-----LYRPPNIGINNQQLSVL 383

QY 430 DQKNETSTQT-----YDSKRNNGHVSAQDSIDQLPETTDEPLEKAYSHQLNYAECLF 483
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 384 DGTEFAYGTSSNLPASVY---RKSGTV---DSLDEIPPNNNVPPRQGFSHRLSHVSMER 437

QY 484 MQDRRGTTI-----PFTWTHRSVDFPNTIDAETITQLPVKAYALSSGASIIIEGPGFTGG 538
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 438 SGFSSSVIIRAPMFSWIHRSAEFNNIADSITQIPAVKGNFLFNG-SVISGPGFTGG 496

QY 539 NLLFLKESNSIAK---FKVTLNSAALLQRYVRIRYASTTNLRLFVQNSNDFLVIYIN 595
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 497 DLVRLNSSGNIIQNGYIEVPFIHFPTSTRYVRVRYASVTPHILNVNMGNSSIFSNVTVP 556

QY 596 KTWKDDDLTYQTFDLATNNGMFGSKNELIIGAESFVSNEKIYIDKIEFIPV 650
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 557 ATATSLDNL--QSSDFGYFESANAFSTSSLGN-IVGVRNFSGTAGVIIDRFEPFIPV 608
```

RESULT 32

S32645

parasporal crystal protein cryIaG1 - Bacillus thuringiensis

C;Species: Bacillus thuringiensis

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

Best Local Similarity 32.8%; Pred. No. 2.7e-47;
Matches 214; Conservative 119; Mismatches 242; Indels 78; Gaps 22;

```
QY 31 DNPSTLEELNYKFLRMTESSTEVLDSNTVDAVGTGIVSVG-----QILGVGVGVPF 84
Db 3 NNPIN-ECIPY-----NCLSNPEVVLGGERIE---TGYPDIDISLSLQFLSEFVPG 53
QY 85 AGALTSFYQSFNTIWI---PSDADPWKAPMAQVEVLIDKKIEYAKSKALAELOGLQNN 140
Db 54 AG-----FVLGLVDIIMGIFGFSQ---WDAPLVQIEQLINQRIIEFARNQAIISRLGLSNL 106
QY 141 FEDYVNALNSWKKTPLSLRSKRSQDRIRELFSQAESHFRNSMPSFAVSKFEVLFLPTIYAQ 200
Db 54 AG-----FVLGLVDIIMGIFGFSQ---WDAPLVQIEQLINQRIIEFARNQAIISRLGLSNL 106
QY 107 YQIYAESFREWEADPTN-PALREEMRIQ--FNDMNSALTTAIPLLAVQNTQVPLLSVYVQ 163
QY 201 AANTHLLLLKDAQVFGEMGYSSDAEFYHRQLKLTQOYTDHCVNMYNYGLNGLRGSTY 260
Db 164 AANLHLSVLKDVSVFGQWGFDAATINSRYNDLTRLIGNTYDYAVRWYNTGLERVMGPD 223
QY 261 DAWYKFNRRREMTLTVLDLIVLPFFYDIRLYSGVKTELTDIFDPIFSLNTLOEYGP 320
Db 224 DMWRYNQFRRELTTLVLDIVLFSNYSRRYPRTVSQLTREIYNPV-----LENFDG 278
QY 321 TFLS-----IENSRKPHLFYLOGIEFHTRLQPGYFGKDSFNWGSNYVETRPSIGSSKT 376
Db 279 SFRGMAQRIEQINRQPHLMDILNSITTYTDVHRG-----FNWWSGHQITASPVGSGPE 332
QY 377 ITSPFYGDK-STEPVQKLSFDGKQVETIAN-----TDVAAMPNGKVLGVTKVDPSQYD 430
Db 333 FAPFLFGMAGNAAPVVLVSUTGLGIFRLTSSPLRYRIILGSGNNOELFLVDGTGTF 392
QY 431 DQNETSTQTYDSKRNNGHVSADSIDQLPETTDEPLEKAYSHQNLNAYAECLMQDRRGT 490
Db 393 LTTNLPST-----LYRQGTV---DSLVDIPPQNSVPPRAGFSHRLSHVT--MLSQAAGA 443
QY 491 I-----PFTWTRSDVFNITDAEKITQLPVVKAYALSSGASIIIEGPGFTGNLLFLKE 545
Db 444 VYLRAPTFWQHSRAEFNIIIPSSQITQIPLKSTNLGSGTSVKGPGTGDIL--RRT 502
QY 546 SSNSIAKFKYTLNSAALLQRYRIRYASTTNLRFLVQ-----NSNNDPLVYINKTMN 599
Db 503 SPQISTLRVNI-TAPLSQRYRIRYASTTNLRFLVQ-----NSNNDPLVYINKTMN 599
QY 600 KDDLTYTQDPLATNSMGFSGDKNELIICAESFVSNKIIYIDKIEFIPVQL 652
Db 556 SGNLQSGSRFTVGTTPFNSGSSVFTLSAHVFNSGNEVYIDRIEFVPAEV 608
```

RESULT 35

S11445
parasporal crystal protein cryIA.c - Bacillus thuringiensis (strain BTS89A) (fragment)
A; Variety: strain BTS89A
C; Date: 21-Nov-1993 #sequence_revision 06-Dec-1996 #text_change 09-Jul-2004
R; Accession: S11445
R; Bardeine, F.; Seurinck, J.; Lambert, B.; Peferoen, M.
Nucleic Acids Res. 18, 5546, 1990
A; Title: Nucleotide sequence and deduced amino acid sequence of a cryIA(c) gene variant
A; Reference number: S11445; MUID: 91016843; PMID: 2216729
A; Accession: S11445
A; Molecule type: DNA
A; Residues: 1-618 <DAR>
A; Cross-references: UNIPROT: Q45737; EMBL: X54159; NID: g40274; PIDN: CAA38098.1; PID: g40275
A; Experimental source: strain BTS89A
A; Note: in the authors' translation 75-Ala is shown after residue 83 and, consequently,
C; Superfamily: parasporal crystal protein
C; Keywords: delta-endotoxin

Query Match 25.3%; Score 861.5; DB 2; Length 618;
Best Local Similarity 33.5%; Pred. No. 2e-47;

Matches 219; Conservative 111; Mismatches 242; Indels 81; Gaps 24;

QY 31 DNPSTLEELNYKFLRMTESSTEVLDSNTVDAVGTGIVSVG-----QILGVGVGVPF 84

```
Db 3 NNPIN-ECIPY-----NCLSNPEVVLGGERIE---TGYPDIDISLSLQFLSEFVPG 53
QY 85 AGALTSFYQSFNTIWI---PSDADPWKAPMAQVEVLIDKKIEYAKSKALAELOGLQNN 140
Db 54 AG-----FVLGLVDIIMGIFGFSQ---WDAPLVQIEQLINQRIIEFARNQAIISRLGLSNL 106
QY 141 FEDYVNALNSWKKTPLSLRSKRSQDRIRELFSQAESHFRNSMPSFAVSKFEVLFLPTIYAQ 200
Db 107 YQIYAESFREWEADPTN-PALREEMRIQ--FNDMNSALTTAIPLLAVQNTQVPLLSVYVQ 163
QY 201 AANTHLLLLKDAQVFGEMGYSSDAEFYHRQLKLTQOYTDHCVNMYNYGLNGLRGSTY 260
Db 164 AANLHLSVLKDVSVFGQWGFDAATINSRYNDLTRLIGNTYDYAVRWYNTGLERVMGPD 223
QY 261 DAWYKFNRRREMTLTVLDLIVLPFFYDIRLYSGVKTELTDIFDPIFSLNTLOEYGP 320
Db 224 DMWRYNQFRRELTTLVLDIVLFSNYSRRYPRTVSQLTREIYNPV-----LENFDG 278
QY 321 TFLS-----IENSRKPHLFYLOGIEFHTRLQPGYFGKDSFNWGSNYVETRPSIGSSKT 376
Db 279 SFRGMAQRIEQINRQPHLMDILNSITTYTDVHRG-----FNWWSGHQITASPVGSGPE 332
QY 377 ITSPFYGDK-STEPVQKLSFDGKQVETIAN-----TDVAAMPNGKVLGVTKVDPSQYD 430
Db 333 FAPFLFGMAGNAAPVVLVSUTGLGIFRLTSSPLRYRIILGSGNNOELFLVDGTGTF 392
QY 431 DQNETSTQTYDSKRNNGHVSADSIDQLPETTDEPLEKAYSHQNLNAYAECLMQDRRGT 490
Db 393 LTTNLPST-----LYRQGTV---DSLVDIPPQNSVPPRAGFSHRLSHVT--MLSQAAGA 443
QY 491 I-----PFTWTRSDVFNITDAEKITQLPVVKAYALSSGASIIIEGPGFTGNLLFLKE 545
Db 444 VYLRAPTFWQHSRAEFNIIIPSSQITQIPLKSTNLGSGTSVKGPGTGDIL--RRT 502
QY 546 SSNSIAKFKYTLNSAALLQRYRIRYASTTNLRFLVQ-----NSNNDPLVYINKTMN 599
Db 503 SPQISTLRVNI-TAPLSQRYRIRYASTTNLRFLVQ-----NSNNDPLVYINKTMN 599
QY 600 KDDLTYTQDPLATNSMGFSGDKNELIICAESFVSNKIIYIDKIEFIPVQL 652
Db 556 SGNLQSGSRFTVGTTPFNSGSSVFTLSAHVFNSGNEVYIDRIEFVPAEV 608
```

RESULT 36

S32649

parasporal crystal protein cryIFa3 - Bacillus thuringiensis
C; Species: Bacillus thuringiensis
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C; Accession: S32649

R; Lambert, B.
submitted to the EMBL Data Library, April 1993
A; Reference number: S32645
A; Accession: S32649
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1174 <LAW>
A; Cross-references: UNIPROT: Q45749; EMBL: Z22512; NID: g295865; PIDN: CAA80235.1; PID: g29586
C; Superfamily: parasporal crystal protein
C; Keywords: delta-endotoxin

Query Match 24.8%; Score 845; DB 2; Length 1174;

Best Local Similarity 33.3%; Pred. No. 5.9e-46;

Matches 198; Conservative 112; Mismatches 220; Indels 64; Gaps 16;

QY 82 VFPAGALTSFYQSFLNTIWPSDADPWKAPMAQVEVLIDKKIEYAKSKALAELOGLQNNF 141

Db 49 VFGVGVAFLDFLIMGFIPTSE---WSFLQLQIEQLIEQRIETLERNRAITTLRLGLADSY 105

QY 142 EDYVNALNSWKKTPLSLRSKRSQDRIRELFSQAESHFRNSMPSFAVSKFEVLFLPTIYAQ 201

Db 106 EYVLEALREWEENP---NNAQLREDVRIRFANTDDALITAINNFTLTISPEILLSVYVQA 162

Db 374 VVEGVR---FLIARDNNLDSLFLY---RKSGTL---DSFTELPPEDESTPPYIGYSHRL 424
Qy 477 NYAE-----CFLMQDRRGITPEFTWTHRSVDFNFNTDAEKITQLPVPVKAYALSSGASIIIE 531
Db 425 CHARFARSPVLEPNFARLPVFWTHRSASPTNEVSPSRITQIPVKAHTLASSASVIK 484
Qy 532 GFGFTGGNLLFLKE--SSNSIAKFVKTLNSAALLQRYVRIRIYASTNRLVLFQNSNDFL 590
Db 485 GFGFTGGDITMNNINLGDGLRTVTV--TGRLPQSYIIRLYASVANSNGVFRHLPOPSY 543
Qy 591 VVIYNKWKDDLYIQFDLATNNSMGFCDKNELIIGAESFVSNEKIYIDKIEFPV 650
Db 544 GISFPRTWGTDEPLTSRSFALTILPTITLTRAQEEF-----NLTIPEGVIDRIEFVVPV 598
RESULT 41
B42459
hypothetical protein 2 (cryIF 3' region) - Bacillus thuringiensis (strain aizawai) (frag
C:Species: Bacillus thuringiensis
C>Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C:Accession: B42459
R:Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C.
J. Bacteriol. 173, 3966-3976, 1991
A:Title: Isolation and characterization of a novel insecticidal crystal protein gene fro
A:Reference number: A42459; MUID:91286178; PMID:2061280
A:Accession: B42459
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-380 <CHA>
A:Cross-references: UNIPROT:Q8KY61; UNIPROT:Q45740; GB:M63897
C:Superfamily: parasporal crystal protein
Query Match 20.6%; Score 700; DB 2; Length 380;
Best Local Similarity 36.6%; Pred. No. 2.2e-37;
Matches 145; Conservative 87; Mismatches 128; Indels 36; Gaps 8;
Qy 1 MNPNNRSEHDTI-----KVTNSELOTHNQYPLADNPNSLTLEELNYKEFLRMTEDSS 53
Db 1 MKLKPNPKHQSFSSNAKVDKISTDS-----LKNETDIELQINIHEDCLKISEYEN 50
Qy 54 TE-VLDNSTVKDAGVTGIVGVGQILVGVVPFAGALTSTFYQSFLNTIPSDADPKAFWA 112
Db 51 VEPFVSASTIQ-----TGISAGKILGLTGVFPAGVASLYSFILGELWPKGNQWEIFME 106
Qy 113 QVEVLIDKKTIEYAKSKALAELOGLQNNFEDYVNALNSWKKTPLSLRSKSQDRIRELFS 172
Db 107 HVEEIIHQISTVARNKALTDLKGLGDALAVYHESLESWVG---NRKNTRRSVKVSQYI 163
Qy 173 QAESHFRNSMPSFAVSKFEVLFLPTVQAQANTHLLLLKDAQVGEWGYSSDVAEFYHR 232
Db 164 ALELMFVOKLPSPFAVSGEEVPLPIYQAQANLHLLLRDASIFGKEWGLSSSEISTFYNR 223
Qy 233 QLKLTQQYTDHCVNWNVYVGLRSGTSDYDAWVKFNRFRREMTLTVLDLIVLPFFYDIR 292
Db 224 QVERAGDYSDHCWKVYSTGLNLRGTNAESWVRYNQPKDNTLMVLDLVALFPSYDTLVY 283
Qy 293 SKGVKTELRDIFTDPIFSLNTLQY-----GTFLSIENS-IRKPHLDYLOGIE 342
Db 284 PIKTSQLTREVTYDAIGTHPNPASFASTTWNNAFSTIESAVVRNPHLLDFLEQVT 343
Qy 343 PHTRLQPGYFGKGSFNWYSGNVYTRPSIGSSKIT 378
Db 344 IYSLLS-RWSNTQYNNMGGHRLFRITGGMLNTST 378

RESULT 42
S19306
parasporal crystal protein cry9Aa1 - Bacillus thuringiensis
A:Alternate names: delta-endotoxin; insecticidal crystal protein; parasporal crystal pro
C:Species: Bacillus thuringiensis
C>Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C:Accession: S19306; S23588; A44847; S14602; S14837
R:Smulevitch, S.V.; Osterman, A.L.; Shevelev, A.B.; Kaluger, S.V.; Karasin, A.I.; Kadyrd

FEBS Lett. 293, 25-28, 1991
A:Title: Nucleotide sequence of a novel delta-endotoxin gene cryIg of Bacillus thuringier
A:Reference number: S19306; MUID:92070568; PMID:1660003
A:Accession: S19306
A:Molecule type: DNA
A:Residues: 1-1156 <SMU>
A:Cross-references: UNIPROT:Q99031; EMBL:X58120; NID:g870929; PIDN:CAAA1122.1; PID:g4027J
A:Experimental source: subsp. galleriae
A:Accession: S23588
A:Molecule type: protein
A:Residues: 24-34 <SMU1>
R:Gleave, A.P.; Hedges, R.J.; Broadwell, A.H.
J. Gen. Microbiol. 138, 55-62, 1992
A:Title: Identification of an insecticidal crystal protein from Bacillus thuringiensis Dε
A:Reference number: A44847; MUID:92211329; PMID:1566556
A:Accession: A44847
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1151 <GLE>
A:Cross-references: EMBL:X58534; NID:g48879; PIDN:CAAA1425.1; PID:g48880
A:Experimental source: isolate DSR517
A:Note: sequence extracted from NCBI backbone (NCBIN:92865, NCBIP:92867)
C:Genetics:
A:Gene: cryIG
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 19.9%; Score 679; DB 2; Length 1156;
Best Local Similarity 28.9%; Pred. No. 2.4e-35;
Matches 197; Conservative 129; Mismatches 292; Indels 64; Gaps 21;
Qy 5 NRSEHDTIKVTPNSELOTNHNQYPLADNPNSLTLEELNYKEFLRMTEDSSTEVLN-NSTVK 63
Db 2 NQNHGILGASGCCASDDVAKYPLANNP-----YSSALNLSNCSQSSILNWINIIG 53
Qy 64 DAVGTGIVSVGQILVGVVPFAGALTSTFYQSFLNTIPSDADPKAFWAQVEVL--IDKK 121
Db 54 DAAKEAVSIGTIVSLITAPSLTGLISIVYDLIGKVLGSGSGQISIDLSICDLSIIDL 113
Qy 122 IEEYAKSKALAELOGLQNNFEDYVNALNSWKKTPLSLRSKSQDRIRELFSQAESHF--- 178
Db 114 VSQSVLNDGIADFNGSVLLYRNYLEALDSWNKNP-----NSASAEELRTRFRIADSEFDRI 169
Qy 179 --RRSMP---SFAVSKFEVLFLPTVQAQANTHLLLLKDAQVGEWGYSSDVAEFYHR 232
Db 170 LTRGSLTNGGSLARQNAQIILLPSFASAFPHELLLRDTRATRYGNWGLYNATPFINYQSK 229
Qy 233 QLKLTQQYTDHCVNWNVYVGLNGL--RGSTYDAWVKFNRFRREMTLTVLDLIVLPFFYDIR 290
Db 230 LVELIELYTDYCVHWYNRGPNELRQRTGSATAWLEFHYRREMTLMVLDIIVASFSLDIT 289
Qy 291 LYSKGVKTELRDIFTDPIFSLNTLQYGPITLS-----IENSIRKPHLEFDYLOGI 341
Db 290 NYPIETDFQLSRVIYTDPIGFVHSSLRGSEWFSFVRANFSDLENAIPNRPSPFLANNM 349
Qy 342 EPHT--RLQPGYFGKGSFNWYSGNVYTRPSIGSSKITTSFPYGDKSPEVQKLSFDQOK 399
Db 350 IISTGSLTLVPSPSTRARVWYGS--RDRISPANSQFTELISGQHTTATQITL---GRN 404
Qy 400 VYRTTANTDVAWPNKGVYLVGVTKVDFQYDDQKNETSTQTYDSK--RNNG--HVSQAQDSI 456
Db 405 IFR----VDSQACNLNDTTYGVNRAVF--YHDASGSGORSVVEGVIRTTGIDNPRVQIN 458
Qy 457 DOLPPETTDPELEKAYSHQIYAECF-----LMQDRRGTIPTFTWTHRSVDFNFNTIDAE 510
Db 459 TVLPGENSDIPTPEDYTHILSTINI.TGSLRQVANSRRSSSLVMYGTHTKSLARNNTINPD 518
Qy 511 KITQLPVVKAYALSSGASIIIEPGTGTGNLLFLKESNSIAKFKYTLNSAALLQRYVRIRI 570
Db 519 RITQIPLTKVDRGTGTGVSYPNDPGFIGGALL--QRTDHGSLGLVLRVQVF--PLHURQQIRIKV 576
Qy 571 RYASTTNLRLFVQNSNNDPLVIYIN--KTMNKDDDLTYQTFDLATNNSNMGFSGDKNELI 628

Db 577 RYASTNIRLSV---NGSFGTISQNLPSRWLGRDLYGSGFAIRFEFTSIRPTASPDQIR 633
QY 629 IGAESFVSNEKIYDKIERIPV 650
Db 634 LTIEPSFIRQEVYVDRIEFIPV 655

RESULT 43

B29838
parapsoral crystal protein - Bacillus thuringiensis subsp. israelensis (fragment)
C/Species: Bacillus thuringiensis subsp. israelensis
C/Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 09-Jul-2004
C/Accession: B29838
R/Thorne, L.; Garduno, F.; Thompson, T.; Decker, D.; Zounes, M.; Wild, M.; Walfield, A.M.
J. Bacteriol. 166, 801-811, 1996
A/Title: Structural similarity between the Lepidoptera- and Diptera-specific insecticidal
A/Reference number: A94672; MUID:86223796; PMID:3011746
A/Accession: B29838
A/Molecule type: DNA
A/Residues: 1-934 <THO>
A/Cross-references: UNIPROT:P05662; GB:M12662; NID:g143228
C/Superfamily: parapsoral crystal protein

Query Match 19.5%; Score 665.5; DB 2; Length 934;
Best Local Similarity 29.0%; Pred. No. 1.3e-34;
Matches 210; Conservative 118; Mismatches 246; Indels 151; Gaps 34;

QY 1 MNP-NRSEHDTTKVTNS-ELQTNHNOYPLANDPNSSTLEELNYKEFLRMTE----- 51
Db 1 MNPYQNKNEYEIFNAPSNGFSGKNNSRYPLANKPNQPLKNTNYKOWLNVCODNQYQGN 60
QY 52 ----SSTEVLDSNVKDAVGTGSGVGOILGWGVRPAGALTSFYOSFLNTIWPSSADPW 107
Db 61 AGNFASETI-----VGVSAGIIVGTMLGAPVLAAGIISFGTLPIFW-QGSDPA 113
QY 108 KAFMAQVEV-----LIDKIEEYAKSKALAELOGLQNNFEDVYNALNSWKTPLSLRSK 161
Db 114 NVQDILLNIGRPQIEIDKNIINVLT-----IVTPIKNQLDKQEPFDKEPA-----RTH 165
QY 162 RSQDRTELFSQAE-----SHFRNSMPFVSKVEFLPYPYQAANTHLLLLKDAQV 214
Db 166 ANAKAVHDLFTTEPIEDKDLMLKNN-----ASYRIPTLPAYAQIATWHLNLLKHAAT 219
QY 215 FGEW-----GYSSDVAEYFHRLK-LTQQYTDHCNVNWNVGLNGLRGSTDYAVKEN 267
Db 220 YNINLQNGINSTFNSNYQGLKQIETIDYCIQYNAGLTWIRTNATWNNY 279
QY 268 RFRREMTLVLDLIVLPFPYDIRLYSGVKTELTDRIDFTDPIFSLNTLOEYGTFLSIEN 327
Db 280 TYRLEMTLVLDLIAIPNPDPEKYPGVKSELIREVYT-----NVNSDPTFTITELN 333
QY 328 SI-RKPHLPYLOGIEFHTR-----LQPGVFGKDSFY-----WS----- 361
Db 334 GLTRNPLFTWINGRFPYTRNSRDLDP-----YDIFSFGNQMAFTHTNDRNIWGAVH 389
QY 362 GNVETRPSIGSKTITSPYGBKSTEPVOKLSFGDKGVKVRTTANTDVAAPNGKVLGV 421
Db 390 GNI-----SQDTSKVP--PYRNK---PIDKVIIVHREYSDI-----IY--- 425
QY 422 TKVDPSQYDDQKNETSTQTYDS--KRNGHVSAQDSIDQLPPTTDEPLEKAYSHOLNYA 479
Db 426 EMIFFNSSSVPRYSNSTIENNYKRTDSYM-----IPKQTKW---NEEYGHTLSYI 474
QY 480 EC-----FLMQDRRGIPPTWTHRSVDPNTDAEKITQLPVPVYKAYALSSGASIEGPG 534
Db 475 KTDNYIFSVVRRERRVA--FSWHTSVDFONTIDLNDITQIHALKALKVSSDSKIVKPG 532
QY 535 FTGNNLLFLKESNSIAKFKVTLNSAALLQRYVRIRYASTTNLRLFVQNSNNDPLVIYI 594
Db 533 HTGGDLVILKSDMDFRVRLKNYS-----RQYQVIRIYA--TNAPKTTVFLTGIDTISVEL 586
QY 595 NKTMNKDD-----DLTYQTDFLAT---TNSNMFGSGDKNEL--IIGAESFVSNEKIYDKI 645

Db 587 PSTSRQNPATDLTYADFGVYTFPRTPVKNKTEGEDTLMLTYGTPNHSYN--IYDKI 644
QY 646 EPIPV 650
Db 645 EPIPI 649

RESULT 44

USB881
parapsoral crystal protein cry4Ba1 [validated] - Bacillus thuringiensis subsp. israelensis
N/Alternate names: delta-endotoxin Bt8; insecticidal protein ISRH3; mosquitocidal 130K p1
C/Species: Bacillus thuringiensis subsp. israelensis
C/Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C/Accession: S00398; J0315; A28541; I39869; I40584
R/Chungjatupornchai, W.; Hoeft, H.; Seurinck, J.; Augschanasombat, C.; Vaeck, M.
Eur. J. Biochem. 173, 9-16, 1988
A/Title: Common features of Bacillus thuringiensis toxins specific for Diptera and Lepid
A/Reference number: S00398; MUID:88185334; PMID:2833395
A/Accession: S00398
A/Molecule type: DNA
A/Residues: 1-1136 <CHU>
A/Cross-references: UNIPROT:P05519; EMBL:X07423; NID:g40353; PIDN:CAA30312.1; PID:g40354
R/Yamanoto, T.; Watkinson, I.A.; Kim, L.; Sage, M.V.; Stratton, R.; Akande, N.; Li, Y.; N
Gene 66, 107-120, 1988
A/Title: Nucleotide sequence of the gene coding for a 130-kDa mosquitocidal protein of Ba
A/Reference number: J0315; MUID:88329719; PMID:2301387
A/Accession: A37587
A/Molecule type: DNA
A/Residues: 1-50, 'D', 52-64, 'S', 66-192, 'PHKCTRMVY', 202-204, 'C', 207-363, 'LVQIYLKFN', 374, 'J
YKFLERQVQNVV', 573-593, 'N', 595-686, 'GIIS', 691-720, 'R', 722-822, 'LIVSVRCA', 833-835, 'WD',
A/Cross-references: GB:M20242; NID:g142737; PIDN:AAA22337.1; PID:g142738
A/Accession: J0315
A/Molecule type: protein
A/Residues: 1-13 <YAZ>
A/Note: the majority of sequence differences are consistent with frameshift errors
R/Tungpradubkul, S.; Settassatien, C.; Panyim, S.
Nucleic Acids Res. 16, 1637-1638, 1988
A/Title: The complete nucleotide sequence of a 130 kDa mosquito-larvicidal delta-endotoxi
A/Reference number: A28541; MUID:88157738; PMID:2831510
A/Accession: A28541
A/Molecule type: DNA
A/Residues: 1-204, 'R', 206-1136 <TUN>
A/Cross-references: EMBL:X07082; NID:g40309; PIDN:CAA30114.1; PID:g40310
R/Sen, K.; Honda, G.; Koyama, N.; Nishida, M.; Neki, A.; Sakai, H.; Hmeno, M.; Komano, M.;
Agric. Biol. Chem. 52, 873-878, 1988
A/Title: Cloning and nucleotide sequences of the two 130 kDa insecticidal protein genes c
A/Reference number: I39869
A/Accession: I39869
A/Status: translated from GB/EMBL/DBDJ
A/Molecule type: DNA
A/Residues: 1-202, 'C', 205-271, 'L', 273-324, 'Y', 326-1136 <RES>
A/Cross-references: GB:D00247; NID:g216287; PIDN:BA0010178.1; PID:g216288
R/Anguthanasombat, C.; Chungjatupornchai, W.; Kertbundit, S.; Luxananil, P.; Settassat
Mol. Gen. Genet. 208, 384-389, 1987
A/Title: Cloning and expression of 130-kd mosquito-larvicidal delta-endotoxin gene of Ba
A/Reference number: I40584; MUID:88038331; PMID:2890080
A/Accession: I40584
A/Status: translated from GB/EMBL/DBDJ
A/Molecule type: DNA
A/Residues: 1-142 <RE2>
A/Cross-references: EMBL:X05692; NID:g40350; PIDN:CAA29174.1; PID:g408121
C/Comment: This protein is toxic to many lepidopteran larvae.
C/Superfamily: parapsoral crystal protein
C/Keywords: delta-endotoxin

Query Match 19.3%; Score 656.5; DB 1; Length 1136;
Best Local Similarity 28.3%; Pred. No. 6.6e-34;
Matches 188; Conservative 140; Mismatches 260; Indels 77; Gaps 24;

QY 27 YPLANDPNSTLEELNYKEFLRMTESSTEVLDSNV-KDAVGTGIVSGQILGVGVPPA 85
Db 5 YPLANDLQSGMKNTNYKDWLANCENNQQYGVNPAINSSSVSTALKVAGAILKFNPP-A 63

```
QY      86 GALTIFYOSFLNTIWPSDADP-----WKAFMAQVEVLIDKKIEEYAKSKALAELOQLQNNF 141
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      64 GTVLTVLSNAVLPILWPTNTPPERVWDFMTNTGNLIDQTVTAYVRTDANAKMTWKDYL 123
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     142 EDYVNALSWKTPPLSLRSKRSQDRIRELFSQASHFRNSMPSPA-VSKFEVLFLPTKYAQ 200
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     124 DQYTTKFTWKREP---NNQSYRTAVITQFNLTSAKLRETAVFYFNLVGYELLLLPYVQ 180
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     201 RANTHLLLLKDAQVGEYSSDAEYFHRQLKLTQYTDHCVNWNVNGVLGRGSTY 260
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     181 VANFNLLLRDGLINAQEWLSARSAGDQYLNWVQYTKETIAHSITWNGLDVLNRKSN 240
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     261 DAWKFNFRPREMTLTVLDLIVLFFPYDIRLY-----SKGVKTELTRDITDPIFSLN 313
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     241 GQWITFNDYKREMTIQVLDILALFASYPDRYPADKIDNTKLSKTEFTREIYITALVESPS 300
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     314 TLQEGVPTFLSTENSI-RKPHLFDYLOGIEFTR-----LQGYFGKDSFNWWSGNYVET 367
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     301 S-----KSTAALEAALTRDVLHFTWLKRVDFWNTIYQDLRPLSANKIGFSTNSAQQE 355
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     368 RPSIGSSKITPGFYGDKSTEPVQKLSFDGQKVYRTIANTDVAAMPNGKVILGVTKVDPS 427
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     356 SGIYSSG-----FGSNLTQIQLNS-----NVYKT-SITDTS-PSNR-----VTKMDFY 399
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     428 QYDD---QKNETSTQYDSKRNN--GHVSAQSIDQLPETTDEPLEKAYSHQLNVAECP 482
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     400 KIDGTLASYNITPTPEGLRTTFFGFSTNEN-----TPNQPTVNDYTHILSYIKTD 451
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     483 LMQDRGTTPTFTWTHRSVDFNTDAEKITOLPVVKAYALSSGASIIIEGPGFTGNNLFL 542
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     452 VI-DYNSNRVSWFAWTHKVIDPNQIYTDAITQVPAVKSNFLATAKVIKPGHGTGDLVA 510
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     543 LKSSNSIAKFKVTLNSAAL---LQRYRVRIRYASTTNLRL---FVQNSNNDPLVIYINK 596
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     511 LFSNGTLGRMEILOCKTSIFNDPSTRSYGLRIRYAANSPIVLNVSVLYQVSRGTTISTES 570
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     597 TNNKOD-----DLTYQTF---DLATNSNMGSGDKNELI---IGNAEFVSNEKIVIDKI 645
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     571 TFSRPNNIITDLKYEFPYKDPFDDAIVPMRLS--SNQLITITAIQPLNMTSNQVNIIDRI 628
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     646 ERTPV 650
      : : : : :
Db     629 EIIP 633

RESULT 45
I39870
parasporal crystal protein ISRH4 - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C:Accession: I39870
R:Gen, K.; Honda, G.; Koyama, N.; Nishida, M.; Neki, A.; Sakai, H.; Himeno, M.; Komano,
Agric. Biol. Chem. 52, 873-878, 1988
A:Title: Cloning and nucleotide sequences of the two 130 kDa insecticidal protein genes
A:Reference number: I39869
A:Accession: I39870
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1180 <RES>
A:Cross-references: UNIPROT:P16480; GB:D00248; NID:g216289; PIDN:BA00179.1; PID:g216290
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match      18.7%; Score 637.5; DB 2; Length 1180;
Best Local Similarity 27.6%; Pred. No. 1.1e-32;
Matches 197; Conservative 129; Mismatches 287; Indels 101; Gaps 28;

QY      1 MNP-NRSEHDTIKVTNS-ELQTNHQYPLANDNSTLEENYKEFLRMTESSTEVLID 58
      ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 MNPQYNKNEYTLNASOKLINISNYTRYFIENSPKQLQSTNYKDWLNWCQNOQYGGD 60
      : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     59 NSTVKDA--VGTGIVSVVGILGVVG--VPPFAGALTFSYQSFLLNTIWPSS--DADPWKAFWA 112
```

```
Db      61 FETFIDSGELSAVTIVGTVLTGFGTTPPLGLALIGF-GTLIPVLPAQOQSNWTSDFIT 119
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     113 QVEVLIDKKIEEYAKSKALAELOQLQNNFEDYVNALSWKKTPLSLRSKRSQDRIRLFS 172
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     120 QTKNIIKKEIASTVISNANKILNRSFNVISYTHNHLKTWENNPN---NPONTQD-VRTQIQ 175
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     173 QAESHFRNSMPSPAVS-----KPEVLFLPTYAQAANTHLLLLKDAQVF-----GE 217
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     176 LVHYHFQNVPELVNPSCPPNPSCDYINILVLSYAQAANLHLTVLNOAVKFEAYLKNNR 235
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     218 EMWYSS--EDVAEYFHRQLKLTQYTDHCVNWNVNGVLGRGSTYDA-----WVKFN 268
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     236 QFDYLEPLTAIDYFVPLTKAIEDYTNVCTYKGLNLIK-TTPDNLNGLNINWNTYNT 294
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     269 FRREMTLTVLDLIVLFFPYDIRLYSKGVKTELTRDITDPIFSLNTLQEGVPTFLSIENS 328
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     295 YRTKMTTAVLDLVALFPNVDVGKYPIGVQSELTREIYQVLNFEESPKYY--DFQYQEDS 352
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     329 I-RKPHLFDYLOGIEFTRLQ--PGYFGKDSFNWWSGNYVETRPSIGSSKITITSPPFYGDK 385
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     353 LTRRPHLFTWLDLSLNFYEKQATTN-----NFTSHYNNMFHYTLNISOSSVFGNHN 405
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     386 STEPVQKLSFDGQKVYRTIANTDVAAMPNGKV--YLGVTKVDF-----YSHILSFIKLSLI 426
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     406 VTDKLSLGL-ATNIIYIFLLN--VISLDNKYLDYNNISKMDFFITNGTRLLEKELTAGS 462
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     427 --SOYDOQNETSTQYDSKRNNGHVSAQSIDQLPETTDEPLEKAYSHQLNVAECPFLM 484
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     463 QGITVDVNNKNTFGLPILKRRENQGNPTLFPTYDN-----YSHILSFIKLSLI 509
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     485 QDRGRT-IPEFTWTHRSVDFNTDAEKITOLPVVKAYALSSGASIIIEGPGFTGNNLFL 543
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     510 PATYKTQVTPANTHSSVDPKNTIYTHLTQIPAVKANSLGTASKVQVPGHGTGDLIDF 569
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     544 KESSNSIAKFKVTLNSAALLQRYRIRYAS--TTNLRFLFVQNSNNDP--LVIVINKTMN 599
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     570 KD-----HFKITQHSNFOQSYFIRIRYASNGSANTRAVINLSIPGVAELGMAINPTFS 623
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     600 KDD--DLTYQTFDLATNSNMGFSQDKN-ELIIGAESFVSNEKIVIDKIEPIV 650
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     624 GTDYTNLKYDFQYLEFSNEVFKFAPNQNISLVRNRSVYTTNTVLIDKIEFLPI 677

RESULT 46
A26858
parasporal crystal protein cry4aai - Bacillus thuringiensis subsp. israelensis
N:Alternate names: parasporal crystal protein cryIVA
C:Species: Bacillus thuringiensis subsp. israelensis
C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: A26858; S48691
R:Ward, E.S.; Ellar, D.J.
Nucleic Acids Res. 15, 7195, 1987
A:Title: Nucleotide sequence of a Bacillus thuringiensis var. israelensis gene encoding a
A:Reference number: A26858; MUID:88015571; PMID:2821500
A:Accession: A26858
A:Molecule type: DNA
A:Residues: 1-1180 <WAR>
A:Cross-references: UNIPROT:P16480; GB:Y00423; NID:g40351; PIDN:CAA68485.1; PID:g40352
A>Note: The authors translated the codon GCA for residue 308 as Thr
R:Nishimoto, T.; Yoshisue, H.; Ihara, K.; Sakai, H.; Komano, T.
FEBS Lett. 348, 249-254, 1994
A:Title: Functional analysis of block 5, one of the highly conserved amino acid sequences
A:Reference number: S48691; MUID:94307434; PMID:7913448
A:Accession: S48691
A:Molecule type: DNA
A:Residues: 667-676 <NIS>
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match      18.6%; Score 634.5; DB 2; Length 1180;
Best Local Similarity 27.5%; Pred. No. 1.8e-32;
Matches 196; Conservative 130; Mismatches 287; Indels 101; Gaps 28;
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|---|-----|---|-----|
| QY | 165 | DRIRELFSQAESHERNSMPSE-----AVSKFE-----VLFLPTAAQANTHLLLKDA | 212 |
| Db | 191 | DRVASRFDTANSGQTOHLPEFKNPMWDENSTOEFKRTSVELTLPMTTATVTHLLHLYEGY | 250 |
| QY | 213 | QVGEWGWYSSSEDAVFYHRQLKLTOQYTDHCVN-----WYNVGLNGLRGSTYDAWV | 264 |
| Db | 251 | IEFMTKWNFHNEQ-----YLNLLKVELQOLHLSVETVRTSFLOFLPLNNRSKSSVNA-- | 304 |
| QY | 265 | KNRFPRFMTLTVLDLIVLPPFYDIRLYSKGVKTELTRIDFTDPIPSLNTLOEYGGTFULS | 324 |
| Db | 305 | -YNYVRNNTVNCLDAATWPTFDTHYHGGGKLDLTRLISD--TAGPIEYTTG---- | 357 |
| QY | 325 | IENSIRKPHLDYLOGIEPHTRLOPGYFGKDSFNYSWGNVYTRPS-----IGSKKITITSPF | 381 |
| Db | 358 | -----DKTSGPE-HSNITP-----NNILDT-PSPTYQHSFVSDSIV | 392 |
| QY | 382 | YGDKSTPEVQKLSFDGQKYRTTIANTDVAAPNGKVYLGVTGVDFSQYDDQNE-----TS | 437 |
| Db | 393 | YSRKELQQLDIATYS-----TNNSNCHPVG--LALSYPDGSRYDYGDNQDPDFTTS | 441 |
| QY | 438 | TQTYDSKR-----NNGHV-SAQDSIDQL-----PPPT | 463 |
| Db | 442 | NNYCHNSYTABITLVNARHLNNAKGLQNVESLVSTVNGSGSGICDAMINYLRPPQT | 501 |
| QY | 464 | T-----DEPLEKAYSHQLNYAECLFMQDRRGTTIPFTTTHRSVDFFNTI | 507 |
| Db | 502 | SKNESRDPDKINVLPIITVTKGTGNGLGVISAVPME-----LVP-----ENVI | 547 |
| QY | 508 | -DAEKITQLPV--VKAYALSSGASIEGPGFT-----GGNLLFKESSNSIAKFKVTL | 557 |
| Db | 548 | GDVNAADTKLPLQLKGFPEPKYSEYNNRGISLVREWINGNNA--VKLSNSQSGVGIQTN | 605 |
| QY | 558 | NSAALLQRYRVRIRVASTNLRLFVQNSNNDFLVIYINKTMKDDLLTQTFDLATTNSN | 617 |
| Db | 606 | QTK--OKYEIRCRYAS-----KGDNN-----VYFNVDLSENPPRNSISFG-STESSV | 649 |
| QY | 618 | MGFSGDKNELI-----IGAESF---VSNE---KIVIDKIEFIP | 649 |
| Db | 650 | VGVQENGKVIKLSITTVIIPAGSFVHVITNQSSDLFLDRIEFVP | 695 |
| RESULT 49 | | | |
| C32053 | | | |
| N:Alternative names: parasporal crystal protein B1 - Bacillus thuringiensis subsp. kurstaki | | | |
| C:Species: Bacillus thuringiensis subsp. kurstaki | | | |
| C:Date: 13-Jul-1989 #sequence_revision 13-Jul-1989 #text_change 09-Jul-2004 | | | |
| C:Accession: C32053; A29913 | | | |
| R:Widner, W.R.; Whiteley, H.R. | | | |
| J. Bacteriol. 171, 965-974, 1989 | | | |
| A:Title: Two highly related insecticidal crystal proteins of Bacillus thuringiensis subsp. | | | |
| A:Reference number: A32053; MUID:89123178; PMID:2914879 | | | |
| A:Accession: C32053 | | | |
| A>Status: preliminary | | | |
| A:Molecule type: DNA | | | |
| A:Cross-references: UNIPROT:P21253 | | | |
| A:Residues: 1-633 <WID> | | | |
| R:Donovan, W.P.; Dankocsik, C.C.; Gilbert, M.P.; Gawron-Burke, M.C.; Groat, R.G.; Carlto | | | |
| J. Biol. Chem. 263, 561-567, 1988 | | | |
| A:Title: Amino acid sequence and entomocidal activity of the P2 crystal protein. An inse | | | |
| A:Reference number: A29913; MUID:88087146; PMID:3121615 | | | |
| A:Accession: A29913 | | | |
| A:Molecule type: DNA | | | |
| A:Residues: 1-587, 'FRY' <DON> | | | |
| C:Genetics: | | | |
| A:Gene: cryBI | | | |
| Query Match 7.2%; Score 245.5; DB 2; Length 633; | | | |
| Best Local Similarity 21.8%; Pred. No. 5.6e-08; | | | |
| Matches 146; Conservative 96; Mismatches 258; Indels 171; Gaps 29; | | | |
| QY | 62 | VKDAVGTGISV-----VGQILG-----VVGVPFAGALTFSFYQSFLNTIWPSDADPWKAFM | 111 |

| | | | |
|--|-----|--|-----|
| Db | 50 | VAPVVGTVSSFLKKVGLSIGRIILSELNGIIFPGSGTNLMQDIIR----- | 95 |
| QY | 112 | AQVEYLIDKKIBEYAKSKALAELOQNFDY-----VNALN-SWKKTPLSLRSKRSQDR | 166 |
| Db | 96 | -ETEQLNQLRLNTDLARVNABELIQLQANIREFNQOVNDFLNPTQNPVPLSITS--SVNT | 152 |
| QY | 167 | IRELSQAESHPNSMPSFAVSKFEVLFLPTAAQANTHLLLKDAQVGEWGWYSSDEV | 226 |
| Db | 153 | WOOL-----FLNLRPQFGYQQLLLPLFAQAANMHLSEFIRDVLNADGWGISAATL | 205 |
| QY | 227 | ABFYHRQLKLTOQYTDHCNVNVLNGLRGSTYDAWKFNFRFREMILTVDLVLVLPDF | 286 |
| Db | 206 | RYRDYRLNYFDYDNYCINTYQTAFRGLNRLHD-----MLEFRTYMLNVEYVYISL | 261 |
| QY | 287 | YDIR-----LVSKGVKTELTRDI-----FTDPIPSLNT-----LOEYGGTFILSIENS | 328 |
| Db | 262 | PKYQSLMVSSGANLYASGGPQQTQSFTAQNPFLYSLFQVNSNYLSLISGSTRLSI--- | 318 |
| QY | 329 | IRKPHLDYLOGIEPHTRLOPGYFGKDSFNYSWGNVYTRPSIGSKKITITSPFYGDKSTE | 388 |
| Db | 319 | -----TFPNIGL-----PGSTTTHLSNARVNY-----SGGVSSGLIGATNLN | 357 |
| QY | 389 | PVQKLSFDGQKYRTTIANTDVAAPNGKVYLGVTGVDFSQYDDQKNETSTQYDYSKRNG | 448 |
| Db | 358 | H-----NFNCSTVLPPLSTPFVRSWLDs---GTDREGVATSNWQTE-SFQITLSLR-CG | 407 |
| QY | 449 | HVSAQDSIDQLPP-----ETTDPL---EKAYSHQLNYAECLFMQDRRGTT---IPFTWT | 497 |
| Db | 408 | AFSARGSNYFPDYFIRNISGVPLVIRNEDLTRPLHYNQIRNIESPGTGGARAYLSV | 467 |
| QY | 498 | HRSDVDFNTIDA-----BKITQLPVVKAVAL-----SSGASIEGPGFTGGNLL | 541 |
| Db | 468 | HNRK---NNIYAANENGTMHAPEDYTGFTISPISHATQVNNQTRTFISEKFGNQDSLR | 524 |
| QY | 542 | FLKESNSIAKFKVPLNSAALLQRYRVRIRVASTNLRLFVQNSNNDFLVIYINKTMKD | 601 |
| Db | 525 | F--EQSNTTARTYLRGNG---NSNLYLRVSSIGNSTIRVTINGRVVTVSNVNTTND | 578 |
| QY | 602 | -----DLTYOTFDL-ATTNSNMGFSGDKNELIIGAESFVSNEKIY | 641 |
| Db | 579 | GVNDNGARFSDINIGNIVASDNTNVTLDINVTLSNGTTFD----- | 618 |
| QY | 642 | IDKIEFIPVOL | 652 |
| Db | 619 | LMNIMFVPTNL | 629 |
| RESULT 50 | | | |
| D32053 | | | |
| parasporal crystal protein B2 - Bacillus thuringiensis subsp. kurstaki | | | |
| C:Species: Bacillus thuringiensis subsp. kurstaki | | | |
| C:Date: 13-Jul-1989 #sequence_revision 13-Jul-1989 #text_change 09-Jul-2004 | | | |
| C:Accession: D32053; S12396 | | | |
| R:Widner, W.R.; Whiteley, H.R. | | | |
| J. Bacteriol. 171, 965-974, 1989 | | | |
| A:Title: Two highly related insecticidal crystal proteins of Bacillus thuringiensis subsp. | | | |
| A:Reference number: A32053; MUID:89123178; PMID:2914879 | | | |
| A:Accession: D32053 | | | |
| A>Status: preliminary | | | |
| A:Molecule type: DNA | | | |
| A:Residues: 1-633 <WID> | | | |
| A:Cross-references: UNIPROT:P21254 | | | |
| R:Dankocsik, C.; Donovan, W.P.; Jany, C.S. | | | |
| Mol. Microbiol. 4, 2087-2094, 1990 | | | |
| A:Title: Activation of a cryptic crystal protein gene of Bacillus thuringiensis subsp. | | | |
| A:Reference number: S12396; MUID:91211618; PMID:2089222 | | | |
| A:Accession: S12396 | | | |
| A:Molecule type: DNA | | | |
| A:Residues: 1-633 <DAN> | | | |
| A:Cross-references: EMBL:X55416; NID:940311; PIDN:CAA39075.1; PID:940312 | | | |

| | | | | | |
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| Query Match | | 7.2% | Score 245; | DB 2; | Length 633; |
| Best Local Similarity | | 19.5% | Pred. No. 6.1e-08; | | |
| Matches 128; | | Conservative 92; | Mismatches 235; | Indels 200; | Gaps 23; |
| Qy | 83 | PFAGALTSF----- | YQSFNTIWPB-DADPWKAFMAQVEVLIDKKIEYAKS | 128 | |
| Db | 52 | PIVGTVASFLKKVGSVLGKRILSELNLIFFPGSTNLMQDILRETEKFLNQRLNTDTLA | 111 | | |
| Qy | 129 | KALAEQLQGNFEDYVNALNSW----- | KKTPLSLRSKRQDRIRELFSQAESHFRNSMP | 183 | |
| Db | 112 | RVNAELTGLQANVEEFNRQVDNPLNPNRNAVPLSITS--SVNTMQQL----- | FLNRLP | 162 | |
| Qy | 184 | SFAVSKEVLFLPTYAAANTHLLLLKDAQVGEENGYSSEDAEFVHROLKLTQQYTDH | 243 | | |
| Db | 163 | QFQMGGYQLLLPLFAQAANLHLSFIRDVILNADENGISAATLRTYRDYLNKNTDYDNY | 222 | | |
| Qy | 244 | CVMWYNVGLGRGSTVDANVKNRPRREMTLVLDLVLFPFYDIR----- | LYSK | 294 | |
| Db | 223 | CINTYOSAFKGLNRLHD----- | MLEPRTYMLNVFEYVSIWSLFKYQSLVSSGANLYAS | 278 | |
| Qy | 295 | GVKTELTRDI----- | FTDPIFSLNT----- | LQEYGTFLSIENSIRKPHLF-- | 335 |
| Db | 279 | GSGPQQTQSFTSQDWPEFLYSLFQVNSYVNLGFSGARLSNTFFNIVGLPGSTTHALLAA | 338 | | |
| Qy | 336 | --DYLOGIEFHTRLQPGYFGKDSFNY----- | | | 359 |
| Db | 339 | RVNYSGGI----- | SSGDIGASPFNQFNCSFTLPLLTFFVRSWLDSGSDREGVATVTN | 392 | |
| Qy | 360 | WSGNYVETRPSI----- | GSKTITSFPGDKSTEPVKLSFDGQKV--YRTIANTDV | 409 | |
| Db | 393 | WQTESFETTLGLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNEIRN--- | 449 | | |
| Qy | 410 | AAPWNG----- | KVVLGVTKVDFSQYDDQKNETSTQTYDSKRNNGHVSAQDS--IDQLPPE | 462 | |
| Db | 450 | IASPSGTGPGARAYM----- | | | 490 |
| Qy | 463 | TTDPELEKAYSHQNYAECLMQDRRGTIPTFTWTHRSVDFFNTIDAEDITQLPVVKAYA | 522 | | |
| Db | 491 | YTGFTISPIHATQVNNQ----- | TRTFISEKFGNGDSLRFEQNNTTARYT | 535 | |
| Qy | 523 | LSSGASIIIEGPGTGGNL-- | LFLKESNSIAKFKVTLNSAALLQRYVRIRYASTTNLRL | 580 | |
| Db | 536 | LRG----- | NGNSYNLYLRVSSIGNSTIRTING----- | RVYTAINVNT | 573 |
| Qy | 581 | FVON----- | SNNDLVIYINKTMNKDDDLTYQTFDLATTN | 615 | |
| Db | 574 | TTNNDGVNDNGARPSDINIGNVASSNSVFLDINVTLNSGTQFDLMNIMLVPTN | 628 | | |

Search completed: February 14, 2005, 15:24:14
Job time : 65 secs

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